

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 05:53:59 ; Search time 3768 Seconds

(without alignments)  
10943.977 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008  
Sequence: 1 agacacactcaaaaagccat.....tagataattagacacatg 1008Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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3:  gb_in:*
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5:  gb_ov:*
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8:  gb_pl:*
9:  gb_pr:*
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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
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19: em_mu:*
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21: em_ov:*
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23: em_pat:*
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36: em_htg_mam:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	1008	6 AR263643	AR263643 Sequence
2	997	98.9	998	6 AR061225	AR061225 Sequence
3	981.6	97.4	1325	6 BD131596	BD131596 Secretory
4	578.4	57.4	96481	9 AC104811	AC104811 Homo sapi
5	575.2	57.1	15736	2 AC060228	AC060228 Homo sapi
6	558	55.4	639	2 BD109282	BD109282 EST and e
7	537.6	53.3	185969	2 AC069037	AC069037 Homo sapi
8	470	46.6	544	6 BD107961	BD107961 EST and e
9	460	45.6	657	6 AR263644	AR263644 Sequence
10	449	44.5	470	6 BD071746	BD071746 Secreted
11	421	41.8	450	6 BD071795	BD071795 Secreted
12	419.4	41.6	185969	2 AC069037	AC069037 Homo sapi
13	339.6	33.7	485	6 BD122986	BD122986 EST and e
14	286.4	28.4	236	6 BD071681	BD071681 Secreted
15	122.6	12.2	259038	2 AC099443	AC099443 Rattus no
16	121.2	12.0	3489	6 AR072952	AR072952 Sequence
17	121.2	12.0	3489	6 AR254713	AR254713 Sequence
18	121.2	12.0	3489	6 AR261360	AR261360 Sequence
19	121.2	12.0	3489	6 AX107938	AX107938 Sequence
20	121.2	12.0	3489	14 KSU52064	US2064 Kaposi's sa
21	121.2	12.0	32207	6 AR065852	AR065852 Sequence
22	121.2	12.0	32207	6 AR127850	AR127850 Sequence
23	121.2	12.0	32207	6 AR194752	AR194752 Sequence
24	121.2	12.0	137508	14 KSU75698	U75698 Kaposi's sa
25	117.8	11.7	28559	14 AP148805	AP148805 Kaposi's
26	116.6	11.6	1365	10 BC049645	BC049645 Mus muscu
27	115.2	11.4	133661	14 U93872	U93872 Kaposi's sa
28	113.4	11.2	158249	2 AL953878	AL953878 Danio rer
29	111.4	11.1	293592	2 AC094571	AC094571 Rattus no
30	111.4	11.0	177100	2 AC112388	AC112388 Rattus no
31	111	11.0	246774	2 AC095078	AC095078 Rattus no
32	110.8	11.0	2931	14 AF192756	AF192756 Kaposi's
33	110.6	11.0	5719	10 MMCATS1	AF051726 Mus muscu
34	110.6	11.0	188880	10 AC092203	AC092203 Mus muscu
35	110.4	11.0	2286	6 AX460942	AX460942 Sequence
36	110.4	11.0	168210	2 AC116700	AC116700 Mus muscu
37	109.6	10.9	224198	2 AC106574	AC106574 Rattus no
38	109.6	10.9	249541	2 AC095672	AC095672 Rattus no
39	109.6	10.9	249774	2 AC126196	AC126196 Rattus no
40	109.4	10.9	272545	2 AC090533	AC090533 Mus muscu
41	109	10.8	182534	10 AC074046	AC074046 Mus muscu
42	108	10.7	186559	10 AL606742	AL606742 Mouse DNA
43	108	10.7	190944	2 AC113108	AC113108 Mus muscu
44	107.8	10.7	178597	10 AL807824	AL807824 Mouse DNA
45	107.8	10.7	238518	2 AC132752	AC132752 Rattus no

## ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	1008 bp	DNA	linear	PAT 29-JAN-2003
AR263643	AR263643	Sequence 1 from patent US 6331413.				
ACCESSION	AR263643					
VERSION	AR263643.1	GI:28075576				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1008)					
AUTHORS	Adler,D.A. and Sheppard,P.O.					
TITLE	Secreted salivary Zs1063 Polypeptide					
JOURNAL	Patent: US 6331413-A 1 18-DEC-2001;					
FEATURES	Location/Qualifiers					



Db	541	CAGGCACACCCTGTGACACTGTAAGCCTGCTGTGACAGGGGCCCCCTGTTGACGTCAGCCTGCTG	600
Oy	606	CAGAAGCACCTGTTGGAGCTGAAGCCTGCTGTGACAGAGCAACCTGTTGACGCTGAGCCTGCTG	665
Db	601	CAGAGGACCACTGTTGGAGCTGAAGCCTGCTGTGACAGAGGCACCTGTTGACGCTGAGCCTGCTG	660
Oy	666	CAGAGGACCACTGTTGGAGTGTGAGAGCGAGTGAGAGGAAACCTTCACACGCTAGCCTGTGA	725
Db	661	CAGAGGACCACTGTTGGAGTGTGAGAGCGAGTGAGAGGAAACCTTCACACGCTAGCCTGTGA	720
Oy	726	CAGCCAAAGCCTGCTGCCCCCAGAACCTCACCCCTTCCCTCTCTTGAAACAGGCAATACAGT	785
Db	721	CAGCCAAAGCCTGCTGCCCCCAGAACCTCACCCCTTCCCTCTCTTGAAACAGGCAATACAGT	780
Oy	786	GAAATCTCTAGAAGATGACATGGGTTCAATTTCTATACTGATGACAAAATPAAGTGAAT	845
Db	781	GAAATCTCTAGAAGATGACATGGGTTCAATTTCTATACTGATGACAAAATPAAGTGAAT	840
Oy	846	CTACAAAAAGTTTTCTTTTCTTTTCCAAAACATATTTCATTCTGTTGATTCAGAGTATTC	905
Db	841	CTACAAAAAGTTTTCTTTTCTTTTCCAAAACATATTTCATTCTGTTGATTCAGAGTATTC	900
Oy	906	TCTCACTCATGATTTGTTGTTGGTAGTTTTTCCCTGGACCTTAATTAATFGAAAAA	965
Db	901	TCTCACTCATGATTTGTTGTTGGTAGTTTTTCCCTGGACCTTAATTAATFGAAAAA	960
Oy	966	CATTGATTAATTAATTAATTAATTAATTAATGATTAATTTAGAC	1002
Db	961	CATTGATTAATTAATTAATTAATTAATTAATTAATTTAGAC	997
RESULT 3			
BDJ31596		1325 bp	DNA linear PAT 18-SEP-2002
LOCUS			
DEFINITION		Secretory proteins and polynucleotides encoding the same.	
ACCESSION	BDJ31596		
VERSION	BDJ31596.1	GI:23226541	
KEYWORDS	JP 2002503634-A/5.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1325)		
AUTHORS	Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Treac,M., Spaulding,V. and Agostino,M.J.		
TITLE	Secretory proteins and polynucleotides encoding the same		
JOURNAL	Patent: JP 2002503634-A 5 05-FEB-2002;		
COMMENT	GENETICS INSTITUTE INC		
	OS Unidentified		
	PN JP 2002503634-A/5		
	PD 05-FEB-2002		
	PF 01-JUL-1998 JP 2000501179		
	PR 02-JUL-1997 US 08/887195 27-OCT-1997 US 08/958304 PI		
	KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE,PI MAURICE TREACY,		
	PI VIKKI SPAULDING,MICHAEL J AGOSTINO		
	PC C07K14/47,A61K38/00,A61P3/10,A61P7/00,A61P7/02,A61P7/04 PC		
	,A61P7/06,A61P11/06.		
	PC A61P17/02,A61P19/02,A61P19/04,A61P19/10,A61P21/00,A61P21/04,		
	PC A61P25/00,		
	PC A61P25/14,A61P25/16,A61P25/28,A61P29/00,A61P31/04,A61P31/10,		
	PC A61P31/12,		
	PC A61P33/00,A61P35/00,A61P35/04,A61P37/04,A61P37/06,A61P37/08,		
	PC A61P37/00,		
	PC C12N5/10,C12N15/09,C12P21/02//A61K39/395,A61K39/395,A61K37/02,		
	PC C12N5/00,		
	PC C12N15/00		
	CC Strandedness: Double;		
	CC Topology: Linear;		
	CC Secretory proteins and polynucleotides encoding the same FH		
Key	Location/Qualifiers		
FT	source		
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	/organism='Unidentified'.		
FEATURES	Location/Qualifiers		

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	Query Match	97.4%; Score 981.6; DB 6; Length 1325;		
	Beat Local Similarity	99.5%; Pred. No. 3.6e-189;		
	Matches 995; Conservative 0; Mismatches 4; Indels 1; Gaps 1			
Oy	10 AAAAAAGCATGATATTCTTTCGTCTCTCTCAAAAGAAGAAAATAATTAATAAATAC	69		
Dd	9 AAAAAAGCAGATATCTTTTGTTTTCTCTCAAGAAAGAAAATATATTTAAAAATAC	68		
Oy	70 ATTGGATTTTCTTAAACAATAATTAATAGTGAATTAATTCATAGGGTCATCAAAAT	129		
Dd	69 ATTTGGATTTTCTTAAACAATAATTAATAGTGAATTAATTCATAGGGTCATCAAAAT	128		
Oy	130 GAAGCTTCTCTTTGGCGCCCTGCATGTATGTGTTCCTTTGCAAGAAAGACGGTTCCC	189		
Dd	129 GAAGCTTCTCTTTGGCGCCCTGCATGTATGTGTTCCTTTGCAAGAAAGACGGTTCCC	188		
Oy	190 CTTGATTTGGTAGAGTAGCAATGACAGATGCCACTTCATTCATCTCTGAATATGCC	249		
Dd	189 CTTGATTTGGTAGAGTAGCAATGACAGATGCCACTTCATTCATCTCTGAATATATCC	248		
Oy	250 TTATGGCATACGGAATTTACCAACCCTCTTTATATGCGCCAGTGAATACAGTCCCCAG	309		
Dd	249 TTAATGGCATACGGAATTTACCAACCCTCTTTATATATGCGCCAGTGAATACAGTCCCCAG	308		
Oy	310 TTACCGTGGGAATTAACACTGACACAGGGTTACCTTGTGATTCCTGTGATTTCTAACCTTC	369		
Dd	309 TTACCGTGGGAATTAACACTGACACAGGGTTACCTTGTGATTCCTGTGATTTCTAACCTTC	368		
Oy	370 TTCCTGATTTCCCTATGCTATCACATCCGCGTTTTCCCTTAGCTACCTGATGAATGT	429		
Dd	369 TCCTGATTTCCCTATGCTATCACATCCGCGTTTTCCCTTAGCTACCTGATGAATGT	428		
Oy	430 TCCTCTCTCCCTCTCTAGGGGTTTTCCGTTTTGTCCCTCTTCAAGSTTTTTTTCAGCAGC	489		
Dd	429 TCCTCTCTCCCTCTCTAGGGGTTTTCCGTTTTGTCCCTCTTCAAGSTTTTTTTCAGCAGC	488		
Oy	490 TGACAGACCCGCTGCCCCACTTATGACGTGAGCTGCGAGCTGCACCTCTTAACAGC	549		
Dd	489 TGACAGACCCGCTGCCCCACTTATGACGTGAGCTGCGAGCTGCACCTCTTAACATC	548		
Oy	550 CACACCTGTAGCAGCTGAGCTGTCTGCAAGGGGCCCTCTGTGACGTGAGCTGTCTGACAGC	609		
Dd	549 CACACCTGTAGCAGCTGAGCTGTCTGCAAGGGGCCCTCTGTGACGTGAGCTGTCTGACAGC	608		
Oy	610 GGACACTGTGAGAGCTGAGCCGTGCGACAGGCACTGTGCGAGCTGAGCCGTGCGACAG	669		
Dd	609 GGACACTGTGAGAGCTGAGCCGTGCGACAGGCACTGTGCGAGCTGAGCCGTGCGACAG	668		
Oy	670 GGACACTGTGAGAGCTGAGCCAGCTGCAGAGGAACTTACACGAGCTGAGCCGTGCTACAGC	729		
Dd	669 GGACACTGTGAGAGCTGAGCCAGCTGCAGAGGAACTTACACGAGCTGAGCCGTGCTACAGC	728		
Oy	730 CAAGCTGCTGCCCAAGAACTCACCCCTTCTCCTCTTGAACAGGCAATCAGTGAAT	789		
Dd	729 CAAGCTGCTGCCCAAGAACTCACCCCTTCTCCTCTTGAACAGGCAATCAGTGAAT	788		
Oy	790 TTCTCTAAGAGTAGTCAATGGGTCAATTTCTATACGTAGACGAATAATGTAATCTAC	849		
Dd	789 TTCTCTAAGAGTAGTCAATGGGTCAATTTCTATACGTAGACGAATAATGTAATCTAC	848		
Oy	850 AAAAGTTTCTTCTTTTCAAAGACTATTTCAATCTGTGTGATTCAGAGTATTCATCTC	909		
Dd	849 AAAAGTTTCTTCTTTTCAAAGACTATTTCAATCTGTGTGATTCAGAGTATTCATCTC	908		
Oy	910 ACTACATTTGATTTGTTTGTGTAGTT-TTTCCTTGGACTTAATTAATGAAAAAATCAT	968		

Dn		909	ACTACATGATTGGTTTGTCGTAGTAACTTCTCGCACTTAATTATAATGAAAAACAAT	968
Oy		969	TGATTAATTAATTAATTAATTAATGAATTAATTTGACCACCATGG	1008
Dn		969	TGATTAATTAATTAATTAATTAATGAATTAATTTGACCACCATGG	1008
RESULT 4				
LOCUS	AC104811	96481 bp	DNA	linear PRI 16-Apr-2002
DEFINITION	Homo sapiens BAC clone RP11-653L5 from 4,			complete sequence.
ACCESSION	AC104811			
VERSION	AC104811.4	GI:19698738		
KEYWORDS	HTC			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	1 (bases 1 to 96481)			
MEDLINE	Sulston,J.E. and Waterston,R.			
PUBMED	Toward a complete human genome sequence			
REFERENCE	Genome Res. 8 (11), 1097-1108 (1998)			
AUTHORS	99063792			
JOURNAL	9847074			
REFERENCE	2 (bases 1 to 96481)			
AUTHORS	Desai,A., Haekenson,W. and Dignan,G.			
JOURNAL	The sequence of Homo sapiens BAC clone RP11-653L5			
REFERENCE	Unpublished (2001)			
AUTHORS	3 (bases 1 to 96481)			
JOURNAL	Waterston,R.H.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (21-Dec-2001) Genome Sequencing Center, Washington			
JOURNAL	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
REFERENCE	MO 63108, USA			
AUTHORS	4 (bases 1 to 96481)			
JOURNAL	Waterston,R.H.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (14-Mar-2002) Genome Sequencing Center, Washington			
JOURNAL	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
REFERENCE	MO 63108, USA			
AUTHORS	5 (bases 1 to 96481)			
JOURNAL	Waterston,R.H.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (24-Mar-2002) Genome Sequencing Center, Washington			
JOURNAL	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
REFERENCE	MO 63108, USA			
AUTHORS	6 (bases 1 to 96481)			
JOURNAL	Waterston,R.H.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (29-Mar-2002) Genome Sequencing Center, Washington			
JOURNAL	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
REFERENCE	MO 63108, USA			
AUTHORS	7 (bases 1 to 96481)			
JOURNAL	Waterston,R.			
REFERENCE	Direct Submiesion			
AUTHORS	Submitted (16-Apr-2002) Department of Genetics, Washington			
JOURNAL	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA			
COMMENT	On Mar 24, 2002 this sequence version replaced gi:19424658.			
	----- Genome Center -----			
	Center: Washington University Genome Sequencing Center			
	Center code: WUGSC			
	Web site: http://genome.wustl.edu/gsc			
	Contact: saplen@watsn.wustl.edu			
	----- Summary Statistics -----			
	Center project name: H_NH0653105			
	-----			
	NOTICE: This sequence may not represent the entire insert of this			
	clone. It may be shorter because we only sequence overlapping			
	clone sections once, or longer because we provide a small overlap			
	between neighboring data submissions.			
	This sequence was finished as follows unless otherwise noted:			

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

**SOURCE INFORMATION:**

The RPCR-1 human BAC library was made from the blood of one male donor, as described by Oosagawa, K., Moon, P. Y., Zhao, B., Frenken, E., Tatenio, M., Catanesi, J. J., and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBAC3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-529K3, 2000 bp overlap; the clone sequenced to the right is RP11-719M16, 2000 bp overlap. Actual end of this clone is at base position 35039 of RP11-719M16.

## FEATURES

**Source**

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	Query Match	Best Local Similarity	Matches	57.4%; 89.1%; 624;	Score 578.4; Pred. 4.8e-107; Conservative 0;	DB 9; Indels 76; Mismatches 0;	Length 96481; Gaps 0;
Oy	199	TTAGAGATGACATATGATGTCACCCATTCATTCATCTCTGTAATATTCCTTATGGCAT	258				
Db	60879	TTAGAGATGACATATGATGTCACCCATTCATTCATCTCTGTAATATTCCTTATGGCAT	60938				
Oy	259	ACGGAAATTTACCACTCTCTTTATTTATTCGCCAGATGAATATACGTCGCCAGTTACCTCGG	318				

[illegible]



QY 319 GAATACCTTACACATGACAGGGTTACCTTGGTATCCCTGATTAATTCTCTGGATT 378  
 DB 35911 GAATACCTTACACATGACAGGGTTACCTTGGTATCCCTGATTAATTCTCTGGATT 35970  
 QY 379 CCCCTATGATCATACATCCCTGGTTTCCCTTACTACTGATGATGTTCTCTCT 438  
 DB 35971 CCCCTATGATCATACATCCCTGGTTTCCCTTACTACTGATGATGTTCTCTCT 36030  
 QY 439 CCCTCTAGAGGGGTTCCCGTTTTCCTCTCTCAAGGTTTTTTTACAGAGCTGACAGACC 498  
 DB 36031 CCCTCTAGAGGGGTTCCCGTTTTCCTCTCTCAAGGTTTTTTTACAGAGCTGACAGACC 36090  
 QY 499 CGCTGCCCCACCTTATGAGAGTGAAGCTGAGCTGAGCTGACACTTTCACAGCACAACCTGT 558  
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 QY 559 AGCAGCTGAGCTGCTGCTGAGAGGGCCCTGTTGACAGCTGAGCTGCTGCTGACAGAGCACTGT 618  
 DB 36151 AGCAGCTGAGCTGCTGCTGAGAGGGCCCTGTTGACAGCTGAGCTGCTGCTGACAGAGCACTGT 36210  
 QY 619 TGAAGCTGAGCTGCTGCTGAGAGGGCACTGTTGACAGCTGAGCTGCTGCTGACAGAGCACTGT 678  
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 DEFINITION EST and encoded human protein.  
 ACCESSION BD109282.1 GI:23204100  
 VERSION JP 2002010789-A/1359.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 639)  
 AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.B.  
 TITLE EST and encoded human protein  
 JOURNAL Patent: JP 2002010789-A 1359 15-JAN-2002;  
 GENSSET CORP  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002010789-A/1359  
 PD 15-JAN-2002  
 PF 07-AUG-2000 JP 2000280989  
 PR 05-AUG-1999 US 60/147499  
 P1 JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI  
 GIORANO  
 PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC  
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 QY 121 AATCAAAATGAAGCTTCTCTTTGGGCTGTCATTTGATAGTTGCTTTTGCAGAGAG 180  
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RESULT 7  
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 REFERENCE 1 (bases 1 to 185969)  
 AUTHORS Birren,B., Linton,L., Nuebaum,C., Lander,E., Abrahams,H., Allen,N.,  
 Anderson,S., Baldwin,J., Baran,N., Baerlein,V., Beda,P.,  
 Birren,B., Linton,L., Nuebaum,C., Lander,E.,  
 2 (bases 1 to 185969)  
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 Homo sapiens chromosome 4, clone RP11-65315  
 Birren,B., Linton,L., Nuebaum,C., Lander,E.,  
 Anderson,S., Baldwin,J., Baran,N., Baerlein,V., Beda,P.,  
 Birren,B., Linton,L., Nuebaum,C., Lander,E.,  
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 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatae,A.,

TITLE  
JOURNAL  
COMMENT

Klein, J., Labrecque, K., Lamazares, R., Landers, T., Lehoczy, J.,  
Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Margolis, N.,  
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Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
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Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Testa, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

Project Information

Center project name: L7416

Center clone name: 653\_L5

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 167163 bases at least Q40

Consensus quality: 175669 bases at least Q20

Consensus quality: 179659 bases at least Q20

Insert size: 188000; agarose-fp

Insert size: 182659; sum-of-contigs

Quality coverage: 3.6 in Q20 bases; agarose-fp

Quality coverage: 3.7 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 34 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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1      1727: contig of 1727 bp in length
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*      1828      3423: contig of 1596 bp in length
*      3424      3523: gap of 100 bp
*      3524      6001: contig of 2478 bp in length
*      6002      6101: gap of 100 bp
*      6102      7881: contig of 1780 bp in length
*      7882      7981: gap of 100 bp
*      7982      10379: contig of 2398 bp in length
*      10380      10479: gap of 100 bp
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*      15913      18292: contig of 2380 bp in length
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*      18393      20550: contig of 2158 bp in length
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## FEATURES

## source

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*      40431      40530: gap of 100 bp
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*      86522      92006: contig of 5485 bp in length
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DB 167886 AATTACCACTCTCTTATATATGCGCCAGTAATACGCCAAGTTACCTGGAGAT 167827
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DB 167826 ACTTACCTGACAGAGGTTACCTTCGATCCCGAATTCCTTCTCGAATTCCTCC 167767
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LOCUS BD107961
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ACCESSION BD107961
VERSION BD107961.1 GI:23202779
KEYWORDS JP 2002010789-A/38.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 544)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 38 15-JAN-2002;
GENSET CORP
COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/38
PD 15-JAN-2002
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PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
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Best Local Similarity 99.8%; Pred. No. 3.1e-85;
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QY 1 AGACAGCTAAAAAGCCATGATTTCTTCTCTCTTAAAAAGAAAAATATATT 60
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SOURCE	unidentified			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 470)			
AUTHORS	Jacobe,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D., Treacy,M., Spaulding,V. and Agostino,M.J.			
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COMMENT	GENETICS INSTITUTE INC			
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	PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI DAVID MERBERG,			
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DEFINITION	Secreted expressed sequence tags (ESTs).				
ACCESSION	BD071795				
VERSION	BD071795.1	GI:22617398			
KEYWORDS	JP 2001519667-A/605.				
SOURCE	unidentified				
ORGANISM	unclassified				
REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 450) Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D., Tracy,M., Spaulding,V. and Agostino,M.J.				
TITLE	Secreted expressed sequence tags (ESTs)				
JOURNAL	Patent: JP 2001519667-A 605 23-OCT-2001; GENETICS INSTITUTE INC				
COMMENT	OS Unidentified PN JP 2001519667-A/605 PD 23-OCT-2001 PF 10-APR-1998 JP 1998543069 PR 10-APR-1997 US 08/838821 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI DAVID MERBERG, PI MAURICE TRACY, VIRKI SPAULDING, MICHAEL J AGOSTINO PC C1N15/12.C1N25/10.C07K14/47.C12Q1/66.A61K38/17 CC Strandedness:				
FEATURES	Double; CC Topology: linear; CC Secreted expressed sequence tags (ESTs) FH Key Location/Qualifiers FT source 1..450 FT Location/Qualifiers Location/Qualifiers 1..450 /organism='unidentified'. /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'				
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Query Match	41.8%; Score 421; DB 6; Length 450;				
Best Local Similarity	100.0%; Pred. No. 2.8e-75;				
Matches 421; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Oy	49 AAAAATAAATTTAAATAATACATTCGCTATTTCTCAAAACAATAATTTATAGTGTAT 108				
Db	21 AAAAATAAATTTAAATAATACATTCGCTATTTCTCAAAACAATAATTTATAGTGTAT 80				
Oy	109 ATTCAATAGGCTCAATCAAAATGAAAGCTTCTCCCTTTGGCCCTGCATTTGATGTGCTTT 168				
Db	81 ATTCAATAGGCTCAATCAAAATGAAAGCTTCTCCCTTTGGCCCTGCATTTGATGTGCTTT 140				
Oy	169 TGCAGAGAAAGACCGCTTCCCTTATTTGGTGAAGATGACATATGACATGCTACCCACT 228				
Db	141 TGCAGAGAAAGACCGCTTCCCTTATTTGGTGAAGATGACATATGACATGCTACCCACT 200				

Qy	229	TATTCATCTCGAATATTCCTTAAGGCAATGGAAATTTACACCTCTCTTATTAATCG	288
Db	201	TATTCATCTCGAATATTTCTTAAGGCAATGGAAATTTACACCTCTCTTATTAATCG	260
Qy	289	CCCAAGTAATACAGTCCCAAGTTACCTCGGAATATCTTACATGACACAGGGTTACCTTC	348
Db	261	CCCAAGTAATACAGTCCCAAGTTACCTCGGAATATCTTACATGACACAGGGTTACCTTC	320
Qy	349	GATATCCCTGGATTTCTAATCTCTCTCGAATTCCTCATGTCTATCACAATCCGATGTTTCC	408
Db	321	GATATCCCTGGATTTCTAATCTCTCTCGAATTCCTCATGTCTATCACAATCCGATGTTTCC	380
Qy	409	CTTAGCTACTCAGTTGAATGTTCTCTCTCTCTCTCTCTCTCTAGGGGTTTCCCGTTTGTCTCTCC	468
Db	381	CTTAGCTACTCAGTTGAATGTTCTCTCTCTCTCTCTCTCTCTAGGGGTTTCCCGTTTGTCTCTCC	440
Qy	469 T	469	
Db	441 T	441	

RESULT 12	
AC069037	
LOCUS	
DEFINITION	AC069037 18596 bp DNA linear HTG 17-MAY-2000
ACCESSION	Homo sapiens chromosome 4 clone RP11-653L5 map 4, WORKING DRAFT
VERSION	AC069037
KEYWORDS	SEQUENCE, 34 unordered pieces.
SOURCE	AC069037.1 GI:7884885
ORGANISM	HTG: HTGS PHASE1; HTGS _DRAFT.
REFERENCE	Homo sapiens (human)
AUTHORS	Homo sapiens
JOURNAL	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 185969)
REFERENCE	Birren, B., Linton, L., Nuebaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-653L5 Unpublished 2 (bases 1 to 185969)
AUTHORS	Birren, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F., Boguslavsky, L., Boukhalter, B., Brown, A., Buckett, G., Campiano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collins, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodgson, S., Domingo, N., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Gargan, J., Gardina, S., Glade, S., Coyette, M., Graham, L., Grland-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A., Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levin, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N., McCarthy, M., McEwan, P., McGuck, A., McKernan, K., MCPheeters, R., Meldrum, J., Meneses, L., Milhova, T., Miranda, C., Mieng, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisanti, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vaasiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted 17-MAY-2000 Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a>
	-- Genome Project --
	Center: Whitehead Institute/ MIT Center for Genome Research
	Center code: WIBR
	Web site: <a href="http://www-seq.wi.mit.edu">http://www-seq.wi.mit.edu</a>
	Contact: <a href="mailto:sequence_submissions@genome.wi.mit.edu">sequence_submissions@genome.wi.mit.edu</a>
	-- Project Information --
	Center project name: L7416

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----- Summary Statistics -----
Center clone name: 653_L5
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175663 bases at least Q40
Consensus quality: 175669 bases at least Q20
Consensus quality: 179699 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 182669; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp
Quality coverage: 3.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1727: contig of 1727 bp in length
1728 1827: gap of 100 bp
1828 3423: contig of 1596 bp in length
3424 3523: gap of 100 bp
3524 6001: contig of 2478 bp in length
6002 6101: gap of 100 bp
6102 7881: contig of 1780 bp in length
7882 7981: gap of 100 bp
7982 10379: contig of 2398 bp in length
10380 10479: gap of 100 bp
10480 13080: contig of 2601 bp in length
13081 13180: gap of 100 bp
13181 15812: contig of 2632 bp in length
15813 15912: gap of 100 bp
15913 18292: contig of 2380 bp in length
18293 18392: gap of 100 bp
18393 20550: contig of 2158 bp in length
20551 20650: gap of 100 bp
20651 24116: contig of 3466 bp in length
24117 24216: gap of 100 bp
24217 27083: contig of 2867 bp in length
27084 27183: gap of 100 bp
27184 31082: contig of 3899 bp in length
31083 31182: gap of 100 bp
31183 36255: contig of 5073 bp in length
36256 36355: gap of 100 bp
36356 40430: contig of 4075 bp in length
40431 40530: gap of 100 bp
40531 44416: contig of 3886 bp in length
44417 44516: gap of 100 bp
44517 48353: contig of 3837 bp in length
48354 48453: gap of 100 bp
48454 52802: contig of 4349 bp in length
52803 52902: gap of 100 bp
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58992 59091: gap of 100 bp
59092 63363: contig of 4272 bp in length
63364 63463: gap of 100 bp
63464 68027: contig of 4564 bp in length
68028 68127: gap of 100 bp
68128 72911: contig of 4784 bp in length
72912 73011: gap of 100 bp
73012 79146: contig of 6135 bp in length
79147 79246: gap of 100 bp
79247 86421: contig of 7175 bp in length
86422 86521: gap of 100 bp
86522 92006: contig of 5485 bp in length
92007 92106: gap of 100 bp
92107 97911: contig of 5805 bp in length
97912 98011: gap of 100 bp
98012 103109: contig of 5098 bp in length
103110 103209: gap of 100 bp

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FEATURES
source
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109912 110011: gap of 100 bp
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119454 119553: gap of 100 bp
119554 126958: contig of 7405 bp in length
126959 127058: gap of 100 bp
127059 134408: contig of 7350 bp in length
134409 134508: gap of 100 bp
134509 143833: contig of 9331 bp in length
143834 143939: gap of 100 bp
143940 155329: contig of 11390 bp in length
155330 155429: gap of 100 bp
155430 168024: contig of 12595 bp in length
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1828. 3423
/feature="assembly_fragment"
3524. 6001
/feature="assembly_fragment"
6102. 7881
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10480. 13080
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13181. 15812
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15913. 18292
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27184. 31082
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36356. 40430
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59092. 63363
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79247. 86421
/feature="assembly_fragment"
86522. 92006
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COMMENT
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PN JP 2002010789-A/15063
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/117499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
CH Key
FI Location/Qualifiers
FT source 1. .485

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      1. .296
        /organism="unidentified"
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Db	1	GGTTTCCCGTTTGTGTCCTTCCTTCAAGGTTTTCCTTACGACGCTGTGACGACCCGCTGCCCCA	60		
OY	509	CCTATTGACGCTGACGCTGCTGCTGACGCTGACCTCTTACAGGCACCACTGTAGACGCTGAG	568		
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OY	569	CCTGCTGACGAGGCGCCCTGTTGACGCTGAGCCTGCTGACGAGGACCTGTTGAGCTGAG	628		
Db	121	CCTGCTGACGAGGCGCCCTGTTGACGCTGAGCCTGCTGACGAGGACCTGTTGAGCTGAG	180		
OY	629	CCTGCTGACGAGGACCTGTTGACGCTGAGCCTGCTGACGAGGACCTGTTGAGCTGAG	688		
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OY	689	CCAGCTGACGAGGACCTTACCAAGCTGAGCCTGCTTACAGCCAAACCT	736		
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RESULT 15					
AC099443/c	259038 bp	DNA	linear	HTG 10-MAY-2003	
LOCUS	AC099443	259038 bp	DNA	linear	HTG 10-MAY-2003
DEFINITION	Rattus norvegicus clone CH230-197D1, *** SEQUENCING IN PROGRESS				
ACCESSION	AC099443				
VERSION	AC099443.5	GI:30521301			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAT; HTGS_ENRICHED.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (bases 1 to 259038)				
AUTHORS	Munhy,D,Marle, Wetzker,M,Lee, Abrazon,S, Adams,C, Alder,J, Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D, Anyalebechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H, Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F, Biewald,K, Blatr,J, Blankenburg,K, Blyth,P, Brown,M, Bryant,N, Bunay,C, Burch,P, Burrell,K, Calderon,B, Cardenas,V, Carter,K, Cavazos,I, Cesaar,H, Center,A, Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J, Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L, Davila,M,L, Davis,C, Davy-Carroll,L, De Ande,C, Dederich,D, Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Divya,K, Diaper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K, Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G, Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foister,P, Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M, Guregeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W, Gunaratne,P, Haaland,W, Hamli,C, Hamilton,C, Hamilton,K, Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J, Hennandes,R, Hines,S, Hildun,S,L, Hodgson,A, Hogues,M, Hollins,B, Howells,S, Huljk,S, Hume,D, Idlebird,D, Jackson,A, Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A, Kapackty,S, Kelly,S, Khan,Z, King,L, Kovar,C, Kowals,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J, Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J, Lorenshewna,L, Louisseg,H, Lozdo,R,J, Lu,X, Ma,J, Maheshwari,M, Mahindaratne,M, Mahmood,M, Malloy,K, Mangum,A, Mangun,B, Mapua,P, Martin,K, Martin,R, Martinez,E, Mawhney,S, McLeod,M,P, McNeill,T,Z, Meenen,E, Milosavljevic,A, Miner,G, Minja,E, Montemayor,D, Moore,S, Morgan,J,K, Morris,K, Morris,S, Mundaea,M, Murphy,M, Natr,L,				

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 259038)  
Worley,K.C.  
Direct Submission  
Submitted (15-NOV-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 259038)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

COMMENT

The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly ('a' contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
Project Information  
Center project name: GIHL  
Center clone name: CH230-197D1  
Summary Statistics  
Assembly program: Atilas 3.0;  
Consensus quality: 233512 bases at least Q40  
Consensus quality: 237879 bases at least Q30  
Consensus quality: 240733 bases at least Q20  
Estimated insert size: 249015; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)) .  
\* NOTE: This is a "working draft" sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

I 244738: contig of 244738 bp in length

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* 244739 244838: gap of unknown length
* 244839 246114: contig of 1276 bp in length
* 246115 246214: gap of unknown length
* 246215 247343: contig of 1129 bp in length
* 247344 247443: gap of unknown length
* 247444 249475: contig of 2032 bp in length
* 249476 249575: gap of unknown length
* 249576 251458: contig of 1883 bp in length
* 251459 251558: gap of unknown length
* 251559 253388: contig of 1830 bp in length
* 253389 253488: gap of unknown length
* 253489 256838: contig of 3350 bp in length
* 256839 256938: gap of unknown length
* 256939 259038: contig of 2100 bp in length.
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## FEATURES

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Location/Qualifiers
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38806. .33987
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## ORIGIN

## Query Match

Best Local Similarity 12.2%; Score 122.6; DB 2; Length 259038;

Matches 218; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

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QY 394 CATCCGTGCTTTTCCTTAGTACTCAGTGAATGTTCTTCCTCCCTCCTAGGAGTTT 453
Db 131745 CATCCGCTCTTTACTGCTGAAGGCCAAGCAAGTGTACCAAGCATACTGACGGCGAAG 131686
QY 454 CCCGTTTGCCTCCCTTCAAGGTTTCTTTCAGACGCTGACGACCCGCTGCCCACTAT 513
Db 131685 CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131626
QY 514 TGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573
Db 131625 TGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131566
QY 574 TGCAGGGGGCCCTGTTGAGCTGAGCTGCTGAGAGGCACTGTTGAGAGCTGAGCTGC 633
Db 131565 TGCAGGGGGCCCTGTTGAGCTGAGCTGCTGAGAGGCACTGTTGAGAGCTGAGCTGC 131506
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QY 694 TGCAGAGGCACTGTTGAGCTGAGCTGCTGAGAGGCACTGTTGAGAGCTGAGCTGC 753
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Db 131385 TCCCTGCTGCTGCTGCTG 131369
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Search completed: January 16, 2004, 08:42:23  
Job time : 3777 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 05:51:13 ; Search time 336 Seconds  
(without alignments)  
8098.314 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008  
Sequence: 1 agcagactaaaagccat.....tagataatagacacatg 1008

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_19Jun03:\*

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25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	1008	24	AA045050 Human zsig63 DNA.
2	1008	100.0	1008	24	ABSS2633 Human encoding human
3	1008	100.0	1008	24	ABSS2633 Human zsig63 cDNA.
4	1008	100.0	1008	25	ABX93594 Human cDNA encoding
5	997	98.9	998	22	AA027729 Human transport pr
6	981.6	97.4	1325	20	AA070740 Human secreted pro
7	896.4	88.9	959	20	AA061352 DNA encoding a hum
8	460	45.6	657	24	AA045051 Human zsig63 degen

9	460	45.6	657	24	ABSS2634
10	460	45.6	657	24	AA020592
11	460	45.6	657	25	ABX93595
12	449	44.5	470	20	AA089597
13	421	41.8	450	20	AA089646
14	286.4	28.4	296	20	AA089532
15	121.2	12.0	3489	21	AA030290
16	121.2	12.0	3489	22	AA082901
17	121.2	12.0	3489	24	ABX93805
18	121.2	12.0	32207	20	AA073805
19	121.2	12.0	137507	19	AA019941
20	106	10.5	5120	22	AA084677
21	100	9.9	1037	21	AA059242
22	100	9.9	1472	21	AA059241
23	99.2	9.8	1159	21	AA059240
24	98.2	9.7	2108	24	AB067774
25	93.6	9.3	397	20	AA089891
26	92.8	9.2	5120	22	AA084677
27	92.4	9.2	1101	22	AA063033
28	92.2	9.1	543	13	AA023092
29	89.8	8.9	877	24	AB011932
30	89.8	8.9	3042	23	AB028445
31	89.8	8.9	5215	23	AB028444
32	88.4	8.8	403	21	ABK10240
33	88.2	8.8	627	23	AA093555
34	87.6	8.7	234	16	AA084832
35	87.6	8.7	1101	22	AA063033
36	86.6	8.6	786	17	AA046148
37	86.6	8.6	786	20	AA021098
38	86.4	8.6	486	22	AA075507
39	85.2	8.5	799	19	AA055831
40	85.2	8.5	1926	22	AA082902
41	85.2	8.5	1926	22	AA082902
42	85.2	8.5	2580	21	AA015454
43	85.2	8.5	2580	24	AA064275
44	85.2	8.5	5452	20	AA090923
45	85.2	8.5	8705	20	AA023778

## ALIGNMENTS

RESULT 1	AA045050	standard; DNA, 1008 BP.
ID	AA045050	
XX	AA045050;	
AC	AA045050;	
XX	27-DEC-2002 (first entry)	
XX	Human zsig63 DNA.	
DE	Human: secreted salivary protein; host defense protein;	
KW	immune modulating factor; antipathogenic; cell-cell signalling molecule;	
KW	growth factor; cytokine; growth factor hormone activity; dental caries;	
KW	infection; tooth decay; periodontal disease; gastrointestinal disease;	
KW	thrush; urinary tract infection; vaginal infection; diabetes; obesity;	
KW	anti-inflammatory; chronic tissue damage; lung dysfunction; resectosis;	
KW	gene therapy; salivary gland dysfunction; prostate gland dysfunction;	
KW	forensic DNA profiling; chondrosarcoma; atherosclerosis; chromosome 4;	
KW	gene; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	128..787
FT		/*tag= a
FT		/product= "Human zsig63 protein"
FT	sig_peptide	128..172
FT		/*tag= b
FT	mat_peptide	173..784
FT		/*tag= c
FT		/product= "Mature human zsig63 protein"

Human secreted sal  
Human zsig63 degen  
Human zsig63 degen  
EST clone CP251.  
EST clone CP116.  
EST clone CP128.  
Kapost's sarcoma-a  
Nucleotide sequenc  
Kapost's sarcoma-a  
KSHV LTR DNA (nucl  
KSHV long unique c  
DNA sequence of hu  
Exons B, C and A o  
Exons D, C, B and  
An EcoRI fragment  
Oesophagus cancer  
Spinocherebellar at  
DNA sequence of hu  
Human cDNA clone H  
Antigen tc-7a gene  
Human polynucleoti  
Drosophila melanog  
Drosophila melanog  
Trinucleotide repe  
DNA encoding novel  
Spinocherebellar at  
Human cDNA clone H  
T. cruzi L195 homo  
TCE coding sequenc  
Polyglutamine trac  
Nucleotide sequenc  
Epstein Barr virus  
EBV tethering prot  
Nucleotide sequenc  
Epstein-Barr virus  
Anti-sense strand  
Vector pshuttle DN

XX US2002090677-A1.  
 XX  
 XX 11-Jul-2002.  
 PD  
 XX  
 XX 03-AUG-2001; 2001US-0922236.  
 PF  
 XX  
 XX 17-MAR-1999; 99US-124820P.  
 PR  
 XX 17-MAR-2000; 2000US-0527345.  
 XX  
 XX  
 PA (ADLER/) ADLER D A.  
 PA (SHEP/) SHEPPARD P O.  
 XX  
 XX  
 PI Adler DA, Sheppard PO;  
 XX  
 XX WPI; 2002-642378/69.  
 DR P-PSDB; AAE27862.  
 DR  
 XX  
 XX Novel secreted salivary polypeptide, zsig63, useful as antimicrobial  
 PT agent for treating microbial infection, dental caries, periodontal  
 PT disease, thrush gastrointestinal disease, and for aiding digestion  
 XX  
 XX Claim 3; Page 27-28, 33pp; English.

The invention relates to human secreted salivary polypeptide designated as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63 can be used in detecting agonists and antagonists of its activity, and is also useful as a host defense polypeptide, immune modulating factor, antipathogenic polypeptide, cell-cell signalling molecule, growth factor, cytokine, or as secreted extracellular matrix associated proteins with growth factor hormone activity. It is useful for treating conditions associated with pathological microbes, including bacterial, fungal and viral infections, for treating dental carries (tooth decay), periodontal disease, thrush and gastrointestinal disease, for treating urinary tract infection, vaginal infection and for preventing infection in skin and other epithelial wounds. zsig63 is useful for establishing normal microflora and protect against pathogenic colonisation and invasion, for treating chronic tissue damage e.g. damage in eximerlites associated with diabetes and useful as anti-inflammatory agents. It is useful as a marker of lung dysfunction, salivary gland dysfunction, or dysfunction of prostate gland. It is also therapeutically useful for aiding digestion. Polynucleotides of the invention are used in gene therapy for increasing or inhibiting zsig63 activity, for detecting abnormalities on human chromosome 4 associated with disease or other human traits and as diagnostics in forensic DNA profiling. Sequences of the invention are useful for stimulating proliferation or differentiation of cardiac myocytes, for proliferation or differentiation of adipocytes and for inhibiting chondrosarcomas, atherosclerosis, reestenosis and obesity. The present sequence is human zsig63 DNA. zsig63 gene is located on chromosome 4.

Sequence 1008 BP, 257 A; 251 C; 193 G; 307 T; 0 other;

Query Match	100.0%	Score 1008;	DB 24;	Length 1008;
Best Local Similarity	100.0%	Pred. No. 3.5e-207;		
Matches 1008; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 AAGACGACGCAAAAAAAGCCAGTATGCTGCTCTCTCTCAAAAAAGAGAAAAATATAATT 60  
|||  
Db 1 AGACGACGCTAAAAAAGCCAGTATGCTCTCTCTCTCAAAAAAGAGAAAAATATAATT 60  
QY 61 TAAAAATACATGCGGTATTTCTTAAACAATAAATTAATAGTATATTCATAGGCTC 120  
|||  
Db 61 TAAAAATACATGCGGTATTTCTTAAACAATAAATTAATAGTATATTCATAGGCTC 120  
QY 121 AATCAAAATGAAGCTTCTCCTTTGGGCGTCGATGTGATGTGTCCTTTGCAGAGAAAG 180  
|||  
Db 121 AATCAAAATGAAGCTTCTCCTTTGGGCGTCGATGTGATGTGTCCTTTGCAGAGAAAG 180  
QY 181 AAGGTTCCCTTCATTTGGTGAAGATGACATGACGATGACGCCACTTCATCATCTCT 240  
|||  
Db 181 AAGGTTCCCTTCATTTGGTGAAGATGACATGACGATGACGCCACTTCATCATCTCT 240

QY	241	GAATATTCCTTAATGGCAATACGGAAATTACACACCTCTCTTAATTATACGGCCAGTGAATAC	300
Db	241	GAATATTCCTTAATGGCAATACGGAAATTACACACCTCTCTTAATTATACGGCCAGTGAATAC	300
QY	301	AGTCCCAAGTAAACCTCGGGAATATCTTACACTGACAAGGGTTACCTTGGTATTCCTGGAT	360
Db	301	AGTCCCAAGTAAACCTCGGGAATATCTTACACTGACAAGGGTTACCTTGGTATTCCTGGAT	360
QY	361	TCTAACTTCTCCTGGAATTCCTCTAATGCTATACATCCGTGGTTTTCCCTTAGCTACTGA	420
Db	361	TCTAACTTCTCCTGGAATTCCTCTAATGCTATACATCCGTGGTTTTCCCTTAGCTACTGA	420
QY	421	GTTGAATGTTCCCTCTCCTCCCTCCCTAGGGGTTTCCCGTTGTGCCCTCTTCAAGTTTTT	480
Db	421	GTTGAATGTTCTCTCTCTCTCCTCCTAGGGGTTTTCCCGTTGTGCCCTCTTCAAGTTTTT	480
QY	481	TTACAGACCTGACAGACCCCGCTGCCCACTAATTGCAAGCTGAAGCTGTGACAGCTGACAC	540
Db	481	TTACAGACCTGACAGACCCCGCTGCCCACTAATTGCAAGCTGAAGCTGTGACAGCTGACAC	540
QY	541	TCTTAACAGCCACACCTGTATAGACAGCTGAAGCTTCTGTGACGGGGCCCTGTGTGACGTGAGCC	600
Db	541	TCTTAACAGCCACACCTGTATAGACAGCTGAAGCTTCTGTGACGGGGCCCTGTGTGACGTGAGCC	600
QY	601	TGCTCAGAGGGACCTGTTGGAGCTGAGGCTGCTGACAGAGGACCTGTGGACAGTGAACC	660
Db	601	TGCTCAGAGGGACCTGTTGGAGCTGAGGCTGCTGACAGAGGACCTGTGGACAGTGAAGCC	660
QY	661	TGCTGCAGAGGGACCTGTTGGAGTGGAGGACAGCTGACAGAGAACTTTCACACAGCTGAGCC	720
Db	661	TGCTGCAGAGGGACCTGTTGGAGTGGAGGACAGCTGACAGAGAACTTTCACACAGCTGAGCC	720
QY	721	TGCTTACAGCCAAAGCTGCTGCTGCCCAAGAACTTACACCTTCTCCCTCTCTTGAACAGGCCAA	780
Db	721	TGCTTACAGCCAAAGCTGCTGCTGCCCAAGAACTTACACCTTCTCCCTCTCTTGAACAGGCCAA	780
QY	781	TCAGAGAAATTCCTAGAGAGATACACAGGGTTCAATTTCTATACGATGACAGAAATAAGT	840
Db	781	TCAGAGAAATTCCTAGAGAGATACACAGGGTTCAATTTCTATACGATGACAGAAATAAGT	840
QY	841	GAATATCTCAAAAAGTTTTCTTCTTTTCCAAAGACATATTCTATCTGTGTATTCAGAGT	900
Db	841	GAATATCTCAAAAAGTTTTCTTCTTTTCCAAAGACATATTCTATCTGTGTATTCAGAGT	900
QY	901	ATTCAATCTCACACTATGATTTGTTGTGGTATGTTTCTTGAGACTTAATTATATTGA	960
Db	901	ATTCAATCTCACACTATGATTTGTTGTGGTATGTTTCTTGAGACTTAATTATATTGA	960
QY	961	AAAAACATTGATTAATTAATAATAAATAGATATTAGACCAATAGG 1008	
Db	961	AAAAACATTGATTAATTAATAATAAATAGATATTAGACCAATAGG 1008	

RESULT 2	
ABSS2633	
ID	ABSS2633 standard; DNA; 1008 BP.
XX	
AC	ABSS2633;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	DNA encoding human secreted salivary protein zslg63.
XX	
KW	Human; secreted salivary protein; zslg63; immunogen; zslg63-cytokine;
KW	antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KW	fungal; viral; infection; salivary gland; anti-microbial; dental caries
KW	tooth decay; periodontal disease; thrush; gastrointestinal disease;
KW	urinary tract infection; vaginal infection; skin infection; microflora;
KW	epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KW	chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KW	incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KW	chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KW	digestion; chromosome 4; gene; ds.

XX	Homo sapiens.	
OS		
XX		
FX	Key	Location/Qualifiers
FT	CDS	128..787
FT		/*tag= a
FT		/product= "Human secreted salivary protein zsig63"
FT	misc_feature	128..784
FT		/*tag= b
FT		/note= "Specifically claimed in claim 3"
FT	misc_feature	173..784
FT		/*tag= c
FT		/note= "Specifically claimed in claim 3"
XX		
XX	US2002081701-A1.	
PD		
XX	27-JUN-2002.	
XX		
PF	03-AUG-2001; 2001US-0922480.	
XX		
XX	17-MAR-1999; 99US-124820P.	
PR	17-MAR-2000; 2000US-0527345.	
XX		
XX	(ADLER/) ADLER D A.	
PA	(SHEP/) SHEPPARD P O.	
XX		
FI	Adler DA, Sheppard PO;	
XX		
DR	WPI; 2002-635468/68.	
DR	P-PSDB; ABG31608.	
XX		
PT	Novel secreted salivary protein, zsig63 and polynucleotide encoding it	
PT	useful for treating microbial infections, inflammatory conditions ,	
PT	dental caries and lung infections associated with cystic fibrosis	
XX		
PS	Claim 3; Page 27-28; 33p; English.	
XX		
XX	The present invention relates to a new secreted salivary protein, zsig63.	
CC	The invention is useful for detecting in a test sample, the presence of	
CC	an antagonist or agonist of zsig63 protein activity. The invention is	
CC	also useful as an immunogen for producing an antibody to zsig63	
CC	polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion	
CC	protein are useful for enhancing in vivo killing of target tissues.	
CC	Pharmaceutical composition comprising purified zsig63 polypeptide are	
CC	useful in the treatment of conditions associated with pathological	
CC	microbes, including bacterial, fungal and viral infections. High	
CC	expression of zsig63 in salivary gland suggests that anti-microbial	
CC	polypeptides are useful for treatment of dental caries (tooth decay),	
CC	periodontal disease, thrush and gastrointestinal disease. Other	
CC	applications can be used in urinary tract infections, vaginal infections,	
CC	prevention of infection in skin and other epithelial wounds. The	
CC	polypeptides can be used to establish normal microflora and protect	
CC	against pathogenic colonisation and invasion. The invention is useful	
CC	when pro-inflammatory activity is desired. Applications for	
CC	such pro-inflammatory activity include the treatment of chronic tissue	
CC	damage, particularly in areas having a limited or damaged vascular system	
CC	e.g., damage in extremities associated with diabetes. Antagonists to	
CC	zsig63 polypeptides may be useful as anti-inflammatory agents. The	
CC	invention is useful for the treatment of patients having incompetent	
CC	immune system, such as AIDS (acquired immunodeficiency syndrome) patients	
CC	or individuals that have undergone chemotherapy, radiation treatment. The	
CC	invention is also useful for the treatment of lung infections associated	
CC	with cystic fibrosis and its agonists or antagonists are useful for	
CC	aiding digestion. The present nucleic acid sequence represents the human	
CC	zsig63 gene located on chromosome 4. This sequence encodes the human	
CC	secreted salivary protein zsig63 of the invention.	
XX		
XX		
SO	Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;	
Query Match	100.0%;	Score 1008; DB 24; Length 1008;
Best Local Similarity	100.0%;	Pred. No. 3.5e-207;
Matches 1008; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

[illegible]

AC AAS20591;  
 XX 23-APR-2002 (first entry)  
 DT  
 XX  
 DE Human zsig63 cDNA.  
 XX  
 KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;  
 KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;  
 KW gastrointestinal disease; urinary tract infection; vaginal infection;  
 KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;  
 KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;  
 KW chronic bronchitis; gene therapy; protein therapy; gene.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH CDS /tag= a  
 FT /start= 128..787  
 FT /product= "Human zsig63"  
 FT  
 EN US6331413-B1.  
 XX  
 XX 18-DEC-2001.  
 PD  
 XX 17-MAR-2000; 2000US-0527345.  
 PF  
 XX 17-MAR-1999; 99US-124820P.  
 PR  
 XX (ZYMO) ZYMOGENETICS INC.  
 PA  
 XX Adler DA, Shepard PO;  
 PI  
 DR WPI; 2002-096707/13.  
 DR P-PSDB; AAU74536.  
 XX  
 PT Polynucleotides encoding salivary proteins useful as anti-microbial  
 PT agents -  
 XX  
 XX Claim 2; Column 47-50; 29pp; English.  
 XX  
 CC The invention relates to a polynucleotide derived from the 4q12-4q13  
 CC region of human chromosome 4 and encoding a zsig63 polypeptide, a  
 CC secreted salivary protein with anti-microbial activity. Due to their  
 CC microbial activity, the sequences can be used in the study of microbial  
 CC infections, e.g. for recombinant production of anti-microbial proteins.  
 CC The sequences can be used in the treatment of tooth decay, periodontal  
 CC disease, thrush, gastrointestinal disease, urinary tract infections,  
 CC vaginal infections, skin infections, epithelial wounds, chronic tissue  
 CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung  
 CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence  
 CC represents cDNA encoding human zsig63.  
 CC  
 SQ Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;

Query Match 100.0%; Score 1008; DB 24; Length 1008;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-207;  
 Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACAGACTAAAGGACCATGATCTTCTCTCTTAAAGAGAAAAATATTAAT 60  
 DB 1 AGACAGACTAAAGGACCATGATCTTCTCTCTTAAAGAGAAAAATATTAAT 60  
 OY 61 TAAATAATCATTGCGTATTTCTTAAACATTAATTTATGTTATATTCATAGGGTC 120  
 DB 61 TAAATAATCATTGCGTATTTCTTAAACATTAATTTATGTTATATTCATAGGGTC 120  
 OY 61 TAAATAATCATTGCGTATTTCTTAAACATTAATTTATGTTATATTCATAGGGTC 120  
 DB 61 TAAATAATCATTGCGTATTTCTTAAACATTAATTTATGTTATATTCATAGGGTC 120  
 OY 121 AATCAAAATGAGCTTCTCTTGGGCGCTGATGTAATCTGCTTTTGAAGAAGAG 180  
 DB 121 AATCAAAATGAGCTTCTCTTGGGCGCTGATGTAATCTGCTTTTGAAGAAGAG 180  
 OY 121 AATCAAAATGAGCTTCTCTTGGGCGCTGATGTAATCTGCTTTTGAAGAAGAG 180  
 DB 121 AATCAAAATGAGCTTCTCTTGGGCGCTGATGTAATCTGCTTTTGAAGAAGAG 180  
 OY 181 ACGGTTCCCTCATTTGGTGGAGATGACATGATGTCACCACTTCATCCATCTCT 240  
 DB 181 ACGGTTCCCTCATTTGGTGGAGATGACATGATGTCACCACTTCATCCATCTCT 240

OY 241 GAATATTCCTTAATGGCATACAGGAATTTACACCTCTCTTTATTTATGCCAGTGAATAC 300  
 DB 241 GAATATTCCTTAATGGCATACAGGAATTTACACCTCTCTTTATTTATGCCAGTGAATAC 300  
 OY 301 AGTCCCAAGTTACCTCGGAAATACCTAATCTGACAGAGGTTACCTTGATCCCTGGAT 360  
 DB 301 AGTCCCAAGTTACCTCGGAAATACCTAATCTGACAGAGGTTACCTTGATCCCTGGAT 360  
 OY 361 TCTAATCTTCTCTGATTTCCCTATGCTATACATACATCCGAGTTTCCCTTACCTACA 420  
 DB 361 TCTAATCTTCTCTGATTTCCCTATGCTATACATACATCCGAGTTTCCCTTACCTACA 420  
 OY 421 GTTAAATGTTCT 480  
 DB 421 GTTAAATGTTCT 480  
 OY 481 TTCAAGAGCTGACAGACCCGCTGCCCCAATTTAGAGCTGAGCTGCTGCTGACCTGAC 540  
 DB 481 TTCAAGAGCTGACAGACCCGCTGCCCCAATTTAGAGCTGAGCTGCTGCTGACCTGAC 540  
 OY 541 TCTTACAGCCACACCTGTTAGAGCTGAGCTGCTGCTGAGGGGCCCCCTGTTGAGCTGAG 600  
 DB 541 TCTTACAGCCACACCTGTTAGAGCTGAGCTGCTGCTGAGGGGCCCCCTGTTGAGCTGAG 600  
 OY 601 TGCTGAGAGGACACCTGTTGAGCTGAGCTGAGCTGCTGAGAGGACCTGTTGAGCTGAG 660  
 DB 601 TGCTGAGAGGACACCTGTTGAGCTGAGCTGAGCTGCTGAGAGGACCTGTTGAGCTGAG 660  
 OY 661 TGCTGAGAGGACACCTGTTGAGCTGAGCTGAGCTGAGAGGACCTGTTGAGCTGAG 720  
 DB 661 TGCTGAGAGGACACCTGTTGAGCTGAGCTGAGCTGAGAGGACCTGTTGAGCTGAG 720  
 OY 721 TGCTGAGAGGACACCTGTTGAGCTGAGCTGAGCTGAGAGGACCTGTTGAGCTGAG 780  
 DB 721 TGCTGAGAGGACACCTGTTGAGCTGAGCTGAGCTGAGAGGACCTGTTGAGCTGAG 780  
 OY 781 TCAGTGAATCTCTAGAGAGTACATGAGGTTATCTTATCTGATGAGAAATAGT 840  
 DB 781 TCAGTGAATCTCTAGAGAGTACATGAGGTTATCTTATCTGATGAGAAATAGT 840  
 OY 841 GAAATCTACAAAGTTTCTTCTTCTTCCAAAGCATATTTGATCTGTTGATTCAGAGT 900  
 DB 841 GAAATCTACAAAGTTTCTTCTTCTTCCAAAGCATATTTGATCTGTTGATTCAGAGT 900  
 OY 901 ATTCAATCTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960  
 DB 901 ATTCAATCTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960  
 OY 961 AAAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008  
 DB 961 AAAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008

RESULT 4  
 ABX93594  
 ID ABX93594 standard; cDNA, 1008 BP.  
 XX  
 XX ABX93594;  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Human cDNA encoding zsig63.  
 XX  
 KW Human; ss; gene; zsig63; adhesion; salivary gland; dental caries;  
 KW periodontal disease; thrush; gastrointestinal disease; epithelial wound;  
 KW urinary tract infection; vaginal infection; skin infection;  
 KW pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;  
 KW lung infection; cystic fibrosis; lung dysfunction; digestive;  
 KW salivary gland carcinoma; pneumocystis carinii infection; emphysema;  
 KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;  
 KW cell culture media; gene therapy; human chromosome 4q12-4q13;  
 KW dentinogenesis imperfecta; dentin dysplasia type II.

XX Homo sapiens. Location/Qualifiers  
XX Key 128..787  
XX CDS /\*tag= a  
FT /product= "zsig63"  
FT /note= "This CDS (minus the stop codon) is claimed in  
FT claim 3"  
FT sig\_peptide 128..172  
FT /\*tag= b  
FT mat\_peptide 173..784  
FT /\*tag= c  
FT /label= Mature\_zsig63  
FT /note= "This region is claimed in claim 3"  
XX US2002173027-A1.  
XX 21-NOV-2002.  
XX 03-AUG-2001; 2001US-0922469.  
XX 17-MAR-1999; 99US-124820P.  
XX 17-MAR-2000; 2000US-0527345.  
XX (ADLER/) ADLER D A.  
XX (SHEP/) SHEPPARD P O.  
XX Adler DA, Shepard PO;  
XX WPI: 2003-328428/31.  
XX P-PSDB; AB008515.  
XX Novel isolated zsig63 polypeptide, member of the adhesin family, useful  
PT for treating dental caries, periodontal disease, thrush,  
PT gastrointestinal disease, urinary tract infections, vaginal infections,  
PT skin infections  
XX Claim 3; Page 26-27; 32pp; English.  
XX The invention relates to an isolated zsig63 polypeptide comprising at  
XX least 90% identity to an amino acid sequence which comprises domain 1 of  
XX zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also  
XX included are the polynucleotide encoding zsig63, a zsig63 expression  
XX vector, a cultured cell comprising the vector and expressing the protein,  
XX a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37,  
XX 38-126, 127-219 or 16-219 of zsig63 and an additional protein), using a  
XX zsig63 reporter gene construct to identify zsig63 agonists, and  
XX producing an anti-zsig63 antibody using zsig63 immunogenic peptides,  
XX zsig63 is useful for detecting in a test sample, the presence of  
XX antagonist of zsig63 protein activity. Zsig63 has antimicrobial  
XX activity and since exhibits high expression in salivary gland, can be  
XX used for treating dental caries, periodontal disease, thrush, and  
XX gastrointestinal disease, urinary tract infections, vaginal infections,  
XX skin infections and other epithelial wounds. The polypeptides can be  
XX used to establish normal microflora and protect against pathogenic  
XX colonization and invasion. Zsig63 can also be used for providing  
XX pro-inflammatory activity for treating chronic, tissue damage  
XX particularly in areas having limited or damaged vascular system, e.g.  
XX in diabetes, and for treating immunocompromised AIDS patients or in  
XX individuals that have undergone chemotherapy, radiation treatment, for  
XX treating lung infections e.g. in cystic fibrosis. Detection of zsig63  
XX polypeptide at relatively high levels in the trachea may indicate that  
XX such polypeptides may serve as a marker of lung dysfunction. Zsig63 is  
XX also useful in diagnosing conditions associated with salivary gland or  
XX lung dysfunction including salivary gland carcinoma, Pneumocystis carinii  
XX infection, emphysema, chronic bronchitis, prostate dysfunctions such  
XX as prostate adenocarcinoma, aiding digestion, and as components of  
XX defined cell culture media and may be used to replace serum that is  
XX commonly used in culture. The DNA is useful in gene therapy applications  
XX to increase or inhibit zsig63 activity, and for detecting abnormalities  
XX on human chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis  
XX imperfecta, and dentin dysplasia type II). Zsig63 is an adhesin family

CC member. The present sequence encodes human zsig63.  
XX Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;  
SQ Query Match 100.0%; Score 1008; DB 25; Length 1008;  
Best Local Similarity 100.0%; Pred. No. 3,5e-207;  
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGACAGACTAAAAAGCATGATCTTCTGTTCTCTCTTAAAGAAAAATATATTT 60  
DB 1 AGACAGACTAAAAAGCATGATCTTCTGTTCTCTCTTAAAGAAAAATATATTT 60  
QY TAAAAATACATGGGATTTTCTTAAACAATTAATTTATAGTGTATATTCATAGGCTC 120  
DB TAAAAATACATGGGATTTTCTTAAACAATTAATTTATAGTGTATATTCATAGGCTC 120  
QY 121 AATCAAAATGAAGCTTCTCTTGGGCTGCAATTTATGTTGCTTTTGCAGAAAG 180  
DB 121 AATCAAAATGAAGCTTCTCTTGGGCTGCAATTTATGTTGCTTTTGCAGAAAG 180  
QY 181 ACGGTTCCCTTCAATGAGAGATGACATGAGATGTCACCCACTTCATCTCT 240  
DB 181 ACGGTTCCCTTCAATGAGAGATGACATGAGATGTCACCCACTTCATCTCT 240  
QY 241 GAATATTCCTTATGGCATAGGAATTTACCACTCTCTTATATGAGGCAATATC 300  
DB 241 GAATATTCCTTATGGCATAGGAATTTACCACTCTCTTATATGAGGCAATATC 300  
QY 301 AGTCCCAAGTTACCTCGGAATATCTTACACTGACACAGGGTTACCTTGTATCC 360  
DB 301 AGTCCCAAGTTACCTCGGAATATCTTACACTGACACAGGGTTACCTTGTATCC 360  
QY 361 TCTACTTCTCTGAGATTCCTTATGCTATACATCCGTTGTTCCCTTACCTAC 420  
DB 361 TCTACTTCTCTGAGATTCCTTATGCTATACATCCGTTGTTCCCTTACCTAC 420  
QY 421 GTTGAATGTTCCCTCTCCCTCTAGGGGTTCCGTTGTTCCCTCTCAAGGTTT 480  
DB 421 GTTGAATGTTCCCTCTCCCTCTAGGGGTTCCGTTGTTCCCTCTCAAGGTTT 480  
QY 481 TTCAAGAGCTGACAGACCCGCTGCCACCTATTCAGAGCTGAGCTGAGCTGAC 540  
DB 481 TTCAAGAGCTGACAGACCCGCTGCCACCTATTCAGAGCTGAGCTGAGCTGAC 540  
QY 541 TCTTACAGCCACACCTGTAGAGCTGAGCTGAGAGGGGCCCTGTTGACGCTGAG 600  
DB 541 TCTTACAGCCACACCTGTAGAGCTGAGCTGAGAGGGGCCCTGTTGACGCTGAG 600  
QY 601 TGCTGACAGAGCACCTGTGAGAGCTGAGCTGAGAGGACCTGTTGACGCTGAG 660  
DB 601 TGCTGACAGAGCACCTGTGAGAGCTGAGCTGAGAGGACCTGTTGACGCTGAG 660  
QY 661 TGCTGACAGAGCACCTGTGAGAGCTGAGCTGAGAGGACCTGTTGACGCTGAG 720  
DB 661 TGCTGACAGAGCACCTGTGAGAGCTGAGCTGAGAGGACCTGTTGACGCTGAG 720  
QY 721 TGCTACAGCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB 721 TGCTACAGCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
QY 781 TCAATGAAATTTCTTAAAGAGTACATGCTTCTTATATGATGAGAAATAGT 840  
DB 781 TCAATGAAATTTCTTAAAGAGTACATGCTTCTTATATGATGAGAAATAGT 840  
QY 841 GAAATCTACAAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
DB 841 GAAATCTACAAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
QY 901 ATTGATCTCACTACATGATTTGTTGTGTAGTTTCTTGTGACTTAATTTATG 960  
DB 901 ATTGATCTCACTACATGATTTGTTGTGTAGTTTCTTGTGACTTAATTTATG 960  
QY 961 AAAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008



```

FT      /*tag= a
FT      /product= "secreted protein clone cp16 1"
FN      MO9901466-A1.
PD      14-JAN-1999.
PE      01-JUL-1998; 98WO-US13813.
PR      27-OCT-1997; 97US-0958304.
PR      02-JUL-1997; 97US-0887195.
PA      (GENY ) GENETICS INST INC.
PI      Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Racie LA;
PI      Spaulding V, Treacy M;
XX      WPI; 1999-105994/09.
DR      P-PSDB; AAM30653.
XX      New polynucleotides encoding secreted human proteins - are derived
FT      from human foetal brain, adult testes, adult brain, foetal kidney,
FT      adult salivary gland, or adult blood cDNA libraries, useful as, e.g.
FT      potential vaccines
XX      Claim 23; Page 70-71; 107pp; English.
XX      The present sequence encodes a human secreted protein from clone
CC      cp16 1, deposited as ATCC 98482. Human secreted protein clone
CC      polynucleotides and proteins are predicted to have biological
CC      activities which would make them suitable for treating, preventing or
CC      ameliorating medical conditions in humans and animals. Suggested
CC      activities include nutritional activity, cytokine and cell
CC      proliferation/differentiation activity, immune stimulating (e.g. as
CC      vaccines) or suppressing activity, haematopoiesis regulating activity,
CC      tissue growth activity, activin/inhibin activity, chemotactic/
CC      chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC      ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC      suppressor activity, and tumour inhibition activity. The polynucleotides
CC      are also stated to be useful for gene therapy.
SQ      Sequence 1325 BP; 407 A; 289 C; 241 G; 388 T; 0 other;
Query Match 97.4%; Score 981.6; DB 20; Length 1325;
Best Local Similarity 99.5%; Pred. No. 1.9e-201;
Matches 995; Conservative 0; Mismatches 4; Indels 1; Gaps 1,
QY      10 AAAAAAGCAGTATCTTTGGTTCCTCTTAAAGAGAAAAATATATTTAAAAATAC 69
DB      9 AAAAAAGCAGTATCTTTGGTTCCTCTTAAAGAGAAAAATATATTTAAAAATAC 68
QY      70 ATTGCGTATTTCTTAAACAATTAATTAAGTGAATTCATAGGGTCAATCAAAAT 129
DB      69 ATTGCGTATTTCTTAAACAATTAATTAAGTGAATTCATAGGGTCAATCAAAAT 128
QY      130 GAAGCTTCTCTTTGGGCGTCGATGTATGTGTTCCTTTTGGCAAGAAAGAGCGGTTCC 189
DB      129 GAAGCTTCTCTTTGGGCGTCGATGTATGTGTTCCTTTTGGCAAGAAAGAGCGGTTCC 188
QY      190 CTTGATGTGTAGAGTGAATGACATGACATGATGATCCCACTTCATCATCTTGAATATTC 249
DB      189 CTTGATGTGTAGAGTGAATGACATGACATGATGATCCCACTTCATCATCTTGAATATTC 248
QY      250 TTATGCGCATAGGAATTTACACACCTCTTTATATATGAGCCAGGAATACAGTCCCGAG 309
DB      249 TTATGCGCATAGGAATTTACACACCTCTTTATATATGAGCCAGGAATACAGTCCCGAG 308
QY      310 TTACCTGTGGAAATCTTACACTGACACAGGGTTACCTTGTATGCCCTGGATTTCTAATTC 369
DB      309 TTACCTGTGGAAATCTTACACTGACACAGGGTTACCTTGTATGCCCTGGATTTCTAATTC 368
QY      370 TCCGGAATCCCGTATGCTATCAATCCGAGTGTTCCTTACGTAATCACTCAAGTGAATGT 429
DB      370 TCCGGAATCCCGTATGCTATCAATCCGAGTGTTCCTTACGTAATCACTCAAGTGAATGT 429

```

Db	369	TCCTGGATTCCCTCTATGCTATACATCCGCTGTTTCCCTTAGCTACCTGATGTAATG	428
Qy	430	TCCTCTCTCCCTCCTAGGAGGTTTCCCGTTGTCTCCCTCAAGGTTTTTTTTCACGAGC	489
Db	429	TCCTCTCTCCCTCCTAGGAGGTTTCCCGTTGTCTCCCTCAAGGTTTTTTTTCACGAGC	488
Qy	430	TGCAGACCCGCTGCCCCACCTATTCAGCTAGGCTGTGAGCTGCACCTCTTACAGC	549
Db	489	TGCAGACCCGCTGCCCCACCTATTCAGCTAGGCTGTGAGCTGCACCTCTTACATC	548
Qy	550	CACACCTGTAGCAGCTGAGCCTGCTGACGAGGCCCCCTGTGTGAGCTGAGCCTGTCAGA	609
Db	549	CACACCTGTAGATGTGAGCCTGCTGACGAGGCCCCCTGTGTGAGCTGAGCCTGTCAGA	608
Qy	610	GGCACCTGTGGAGCTGAGCCTGCTGACAGGACCCTGTGGAGCTGAGCCTGTCAGA	669
Db	609	GGCACCTGTGGAGCTGAGCCTGCTGACAGGACCCTGTGTGAGCTGAGCCTGTCAGA	668
Qy	670	GGCACCTGTGGAGCTGAGCCTGCTGACAGGACCCTTACCAAGCTGAGCCTGCTACAGC	729
Db	669	GGCACCTGTGGAGCTGAGCCTGCTGACAGGACCCTTACCAAGCTGAGCCTGCTACAGC	728
Qy	720	CAAGCCTCTGCCCCCAGAACCTCACCCCTTCCCTCTCTTGAACAGGCAAACTGAGAAA	789
Db	729	CAAGCCTCTGCCCCCAGAACCTCACCCCTTCTCTCTCTTGAACAGGCAAACTGAGAAA	788
Qy	790	TTCTCTAGAAGAGTACCATGGGTTTCATTTCTATCTAGTACGAGAAATAGATGATCTAC	849
Db	789	TTCTCTAGAAGAGTACCATGGGTTTCATTTCTATCTAGTACGAGAAATAGATGATCTAC	848
Qy	850	AAAAGTTTTCTTTCTTTTCCAAAGCTATTTTATTTCTGTGTATTCAGAGTATTCATCTC	909
Db	849	AAAAGTTTTCTTTCTTTTCCAAAGCTATTTTATTTCTGTGTATTCAGAGTATTCATCTC	908
Qy	910	ACTACATGATTTGTTGTGNGGTAGTT- TTTCCCTGAGCTTAATTTATTTGAAAAAATCAT	968
Db	909	ACTACATGATTTGTTGTGTGTAGTTATTTCTTGGACTTAATTTTATTTGAAAAAATCAT	968
Qy	969	TGATTAATTAATAATAATAATAGATTAATTTAGACCAATGG	1008
Db	969	TGATTAATTAATAATAATAATAGATTAATTTAGACCAATGG	1008
RESULT 7			
AAx61352			
ID	AAx61352	standard; cDNA; 959 BP.	
AC	AAx61352;		
XX			
AC			
DT	14-JUL-1999	(first entry)	
XX			
DE	DNA encoding a human secreted protein.		
XX			
KM	Human secreted protein; cancer; tumour; neurodegenerative disorder;		
KM	developmental abnormality; fetal deficiency; blood disorder; leukemia;		
KM	immune system disease; autoimmune disease; hepatic disease;		
KM	renal disease; lymphoma; inflammation; allergy; ischemic shock;		
KM	Alzheimer's; cognitive disorder; schizophrenia; prostate disease;		
KM	osteolytic; osteoclast; osteoporosis; arthritis; malignancy; testes disease;		
KM	lung disease; thymus disease; digestive disorder; endocrine disorder;		
KM	infection; AIDS; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W09922243-A1.		
XX			
PD	06-MAY-1999.		
XX			
PF	23-OCT-1998;	98WO-US22376.	
XX			
PR	24-OCT-1997;	97US-0063387.	
PR	24-OCT-1997;	97US-0062784.	
PR	24-OCT-1997;	97US-0063088.	



PR 24-OCT-1997; 97US-0063089.  
 PR 24-OCT-1997; 97US-0063090.  
 PR 24-OCT-1997; 97US-0063091.  
 PR 24-OCT-1997; 97US-0063092.  
 PR 24-OCT-1997; 97US-0063097.  
 PR 24-OCT-1997; 97US-0063098.  
 PR 24-OCT-1997; 97US-0063099.  
 PR 24-OCT-1997; 97US-0063100.  
 PR 24-OCT-1997; 97US-0063101.  
 PR 24-OCT-1997; 97US-0063109.  
 PR 24-OCT-1997; 97US-0063110.  
 PR 24-OCT-1997; 97US-0063111.  
 PR 24-OCT-1997; 97US-0063148.  
 PR 24-OCT-1997; 97US-0063386.  
 (HDMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 PI Brewer LA, Carter KC, Duan DR, Ebner R, Endress GA;  
 PI Feng P, Florence C, Florence KA, Greene JM, Janat F;  
 PI Kaye H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;  
 PI Ruben SM, Shi Y, Soppet DR, Wei Y, Young P;  
 XX  
 DR WPI; 1999-303069/25.  
 DR P-PSDB; AAY19472.  
 XX  
 PT New isolated human genes and the secreted polypeptides they encode  
 XX  
 PS Claim 3, Page 328-329; 546pp; English.  
 XX  
 CC The specification describes cDNA sequences (AAX61322-X61470) encoding  
 CC human secreted proteins (AAY19442-Y19590). The polynucleotides and their  
 CC corresponding secreted polypeptides are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g. by protein or gene therapy.  
 CC Pathological conditions can also be diagnosed by determining the amount  
 CC of the polypeptides in a sample or by determining the presence of  
 CC mutations in the polynucleotides. Specific uses are described for each  
 CC of the polynucleotides, based on which tissues they are most highly  
 CC expressed in, and include developing products for the diagnosis or  
 CC treatment of cancer, tumours, neurodegenerative disorders, developmental  
 CC abnormalities and fetal deficiencies, blood disorders, leukemias,  
 CC diseases of the immune system, autoimmune diseases, hepatic and renal  
 CC diseases, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's  
 CC and cognitive disorders, schizophrenia, prostate diseases, obesity,  
 CC disorders involving osteoclasts such as osteoporosis, arthritis or  
 CC malignancies, diseases of testes, lung or thymus, digestive/endocrine  
 CC disorders, infections and AIDS. The polypeptides are also useful for  
 CC identifying their binding partners.  
 CC  
 XX  
 SQ Sequence 959 BP; 240 A; 245 C; 187 G; 286 T; 1 other;  
 Query Match 88.9%; Score 896.4; DB 20; Length 959;  
 Best Local Similarity 98.8%; Pred. No. 3.5e-183;  
 Matches 923; Conservative 1; Mismatches 7; Indels 3; Gaps 2;

QY 375 GATTCCCTATGTCTATACATCCGTTGTTTCCCTTAGCTACTCAGTTGAATGTTCTC 434  
 Db 312 GATTCCCTATGTCTATACATCCGTTGTTTCCCTTAGCTACTCAGTTGAATGTTCTC 371  
 QY 435 CTCTCCCTCTTGAAGGGGTTTCCGTTTGTCTCTCTTCAAGTTTCTTTCACAGCTGAG 494  
 Db 372 CTCTCCCTCTTGAAGGGGTTTCCGTTTGTCTCTCTTCAAGTTTCTTTCACAGCTGAG 431  
 QY 495 CACCCGCTGCCCACTATTTGACAGCTGAGCTGCTGACAGCTGCACTCTTACAGCCAC 554  
 Db 432 CACCCGCTGCCCACTATTTGACAGCTGAGCTGCTGACAGCTGCACTCTTACAGCCAC 491  
 QY 555 CTGTAGACGCTGAGCCCTGCTGAGAGGGCCCTGTGTGACGCTGAGCCCTGCTGAGAGCC 612  
 Db 492 CTGTAGACGCTGAGCCCTGCTGAGAGGGCCCTGTGTGACGCTGAGCCCTGCTGAGAGCC 551  
 QY 613 ACCTGTTGAGAC-TGAGCCTGCTGACAGAGGACCTGTTGACAGCTGAGCTGCTGAGAG 671  
 Db 552 ACCTGTTGAGCTTGAAGCTGCTGCTGACAGAGGACCTGTTGACAGCTGAGCTGCTGAGAG 611  
 QY 672 CACCTGTTGAGTGAAGGACGCTGACAGAGAACCTTCAACAGCTGAGCTGCTTACAGCA 731  
 Db 612 CACCTGTTGAGTGAAGGACGCTGACAGAGAACCTTCAACAGCTGAGCTGCTTACAGCA 671  
 QY 732 AGCCTGCTGCCCAAGAACCTTCAACCTTCTCTCTCTTGTGAACAGGCAAAATGAGAAAT 791  
 Db 672 AGCCTGCTGCCCAAGAACCTTCAACCTTCTCTCTCTTGTGAACAGGCAAAATGAGAAAT 731  
 QY 792 CTCTAGAAGAGTACCAATGAGTTCTTCTACTGATGACAGAAATGAGAAATCTTCA 851  
 Db 732 CTCTAGAAGAGTACCAATGAGTTCTTCTACTGATGACAGAAATGAGAAATCTTCA 791  
 QY 852 AAGTTTCTTCTTCTTCCAAAGACTATTCTCTGTGTATTTAGAGTATTCATCTCAC 911  
 Db 792 AAGTTTCTTCTTCTTCCAAAGACTATTCTCTGTGTATTTAGAGTATTCATCTCAC 851  
 QY 912 TACATGATTTGTTGTGAGTATTTTCTTCTGACTTAATTTATTTGAAAAAATTTGA 971  
 Db 852 TACATGATTTGTTGTGAGTATTTTCTTCTGACTTAATTTATTTGAAAAAATTTGA 911  
 QY 972 TAATTAATAATAATAATAATAGATAATTTAGACCAA 1005  
 Db 912 TAATTAATAATAATAATAATAGATAATTTAGACCAA 945  
 RESULT 8  
 AAD45051  
 ID AAD45051 standard; DNA; 657 BP.  
 XX  
 AC AAD45051;  
 XX  
 DT 27-DEC-2002 (first entry)  
 XX  
 DE Human zslg63 degenerate DNA.  
 XX  
 XX Human; secreted salivary protein; zslg63 protein; host defense protein;  
 XX immune modulating factor; antipathogenic; cell-cell signalling molecule;  
 XX growth factor; cytokine; growth factor hormone activity; dental caries;  
 XX infection; tooth decay; periodontal disease; gastrointestinal disease;  
 XX thrush; urinary tract infection; vaginal infection; diabetes; obesity;  
 XX anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;  
 XX gene therapy; salivary gland dysfunction; prostate gland dysfunction;  
 XX forensic DNA profiling; chondrosarcoma; atherosclerosis; chromosome 4;  
 XX gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2002090677-A1.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 03-AUG-2001; 2001US-0923236.



[illegible]

PS Claim 4; Page 28-29; 33pp; English.

XX The present invention relates to a new secreted salivary protein, zsig63.  
 CC The invention is useful for detecting in a test sample, the presence of  
 CC an antagonist or agonist of zsig63 protein activity. The invention is  
 CC also useful as an immunogen for producing an antibody to zsig63  
 CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion  
 CC proteins are useful for enhancing in vivo killing of target tissues.  
 CC Pharmaceutical composition comprising purified zsig63 polypeptide are  
 CC useful in the treatment of conditions associated with pathological  
 CC microbes, including bacterial, fungal and viral infections. High  
 CC expression of zsig63 in salivary gland suggests that anti-microbial  
 CC polypeptides are useful for treatment of dental caries (tooth decay),  
 CC periodontal disease, thrush and gastrointestinal disease. Other  
 CC applications can be used in urinary tract infections, vaginal infections,  
 CC prevention of infection in skin and other epithelial wounds. The  
 CC polypeptides can be used to establish normal microflora and protect  
 CC against pathogenic colonisation and invasion. The invention is useful  
 CC when pro-inflammatory activity is desired. Applications for  
 CC such pro-inflammatory activity include the treatment of chronic tissue  
 CC damage, particularly in areas having a limited or damaged vascular system  
 CC e.g., damage in extremities associated with diabetes. Antagonists to  
 CC zsig63 polypeptides may be useful as anti-inflammatory agents. The  
 CC invention is useful for the treatment of patients having incompetent  
 CC immune system, such as AIDS (acquired immunodeficiency syndrome) patients  
 CC or individuals that have undergone chemotherapy, radiation treatment. The  
 CC invention is also useful for the treatment of lung infections associated  
 CC with cystic fibrosis and its agonists or antagonists are useful for  
 CC aiding digestion. The present nucleic acid sequence encodes the human  
 CC secreted salivary protein zsig63 of the invention.

XX Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;

Query Match 45.6%; Score 460; DB 24; Length 657;  
 Best Local Similarity 61.0%; Pred. No. 2.2e-89;  
 Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

OY 128 ATGAAGCTTCCTTGGGCGCTGATGATGTTGCTTTGGCAAGAGACGGTTC 187  
 DB 1 ATGAARYNTYNTYNTGGCCTGATGATGTTGCTTTGGCAAGAGACGGTTC 60  
 OY 188 CCTTCATTTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 247  
 DB 61 CCTTTAHHGNGARGAAGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 OY 248 CCTTATGGCATACGGAATTTACCACTCTCTTATATGCGCAGTGAATACGTC 307  
 DB 121 CATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 OY 308 AGTTACCTGGGATATCTTACCTGATGATGATGATGATGATGATGATGATGAT 367  
 DB 181 WSNATYCCNGGAAATACATGATGATGATGATGATGATGATGATGATGATGAT 240  
 OY 368 TCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 427  
 DB 241 WSNCCNGATTTTCTTATGATGATGATGATGATGATGATGATGATGATGAT 300  
 OY 428 GTTCA 487  
 DB 301 GTTCCGCTCA 360  
 OY 488 GCTGACAGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547  
 DB 361 GCGNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 420  
 OY 548 GCGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 607  
 DB 421 GCGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 OY 608 GAGGACCTGTTGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667  
 DB 481 GARGCNCNGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 540

OY 668 GAGGACCTGTTGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727  
 DB 541 GARGCNCNGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 600  
 OY 728 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 784  
 DB 601 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657

# RESULT 10

AAS20592  
 ID AAS20592 standard; cDNA; 657 BP.

XX AAS20592;

DT 23-APR-2002 (first entry)

XX Human zsig63 degenerate cDNA coding sequence.

XX Human; zsig63; chromosome 4q12-q13; salivary protein; antimicrobial; ss;  
 KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;  
 KW gastrointestinal disease; urinary tract infection; vaginal infection;  
 KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;  
 KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;  
 KW chronic bronchitis; gene therapy; protein therapy; gene.

OS Homo sapiens.

PN US633413-B1.

PD 18-DEC-2001.

PF 17-MAR-2000; 2000US-0527345.

PR 17-MAR-1999; 99US-124820P.

PA (ZYMO) ZYMOGENETICS INC.

PI Adler DA, Sheppard PO;

DR WPI; 2002-096707/13.

XX Polynucleotides encoding salivary proteins useful as anti-microbial  
 PT agents -

XX Claim 3; Column 51-52; 29pp; English.

PS The invention relates to a polynucleotide derived from the 4q12-q13  
 CC region of human chromosome 4 and encoding a zsig63 polypeptide, a  
 CC secreted salivary protein with anti-microbial activity. Due to their  
 CC microbial activity, the sequences can be used in the study of microbial  
 CC infections, e.g. for recombinant production of anti-microbial proteins.  
 CC The sequences can be used in the treatment of tooth decay, periodontal  
 CC disease, thrush, gastrointestinal disease, urinary tract infections,  
 CC vaginal infections, skin infections, epithelial wounds, chronic tissue  
 CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung  
 CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence  
 CC represents a degenerate cDNA encoding human zsig63.

XX Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;

Query Match 45.6%; Score 460; DB 24; Length 657;  
 Best Local Similarity 61.0%; Pred. No. 2.2e-89;  
 Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

OY 128 ATGAAGCTTCCTTGGGCGCTGATGATGTTGCTTTGGCAAGAGACGGTTC 187  
 DB 1 ATGAARYNTYNTYNTGGCCTGATGATGTTGCTTTGGCAAGAGACGGTTC 60  
 OY 188 CCTTCATTTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 247  
 DB 61 CCTTTAHHGNGARGAAGATGATGATGATGATGATGATGATGATGATGATGAT 120









301 AGTCCCAGTTACCCCTGGGATACTTACACTGACACAGGGTTACCTTCGTATCCCTGGAT 36

```

Db      301 AGTCCCACTTACCTGGGAATCTTACACTGACACAGGGTTACTTGTGATCCTGAT 360
Qy      361 TCTAATCTTCTCTGATTTCCCTATGCTATACATCCGTGGTTTCCCTTAGCTACTCA 420
Db      361 TCTAATCTTCTCTGATTTCCCTATGCTATACATCCGTGGTTTCCCTTAGCTACTCA 420
Qy      421 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db      421 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Qy      481 TTCACAGCTGACAGACCCGCTGCCCACTATTGACAGCTGACCTGCTGACCTGAC 540
Db      481 TTCACAGCTGACAGACCCGCTGCCCACTATTGACAGCTGACCTGCTGACCTGAC 540
Qy      541 TCTTACAGCCACCTGTTAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 600
Db      541 TCTTACAGCCACCTGTTAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 600
Qy      601 TGTCTGACAGAGCACTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 660
Db      601 TGTCTGACAGAGCACTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 660
Qy      661 TGTCTGACAGAGCACTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 720
Db      661 TGTCTGACAGAGCACTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 720
Qy      721 TGTCTGACAGAGCACTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 780
Db      721 TGTCTGACAGAGCACTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 780
Qy      781 TCAAGGAAATTTCTTGAAGAGTACAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 840
Db      781 TCAAGGAAATTTCTTGAAGAGTACAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 840
Qy      841 GAAATCTCAAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db      841 GAAATCTCAAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Qy      901 ATTCAATCTCACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 960
Db      901 ATTCAATCTCACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 960
Qy      961 AAAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008
Db      961 AAAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008

```

## RESULT 2

```

US-09-527-345-3
; Sequence 3, Application US/09527345
; Patent No. 6331413
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZS163 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/527,345
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate polynucleotide sequence for zs163
; NAME/KEY: misc. feature
; LOCATION: (1)...(657)
; OTHER INFORMATION: n = A,T,C or G
US-09-527-345-3

```

```

Query Match      45.6%; Score 460; DB 4; Length 657;
Beet Local Similarity 61.0%; Pred. No. 5,6e-102;
Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

Qy      128 ATGAAGCTTCTCTTGGGCTGCTGATGATGTTGCTTCTTGAAGAGAGAGCGGTT 187
Db      1 ATGAARTNTNTNTNTGGGCGTGAATGATGATGATGATGATGATGATGATGATGATGAT 60

Qy      188 CCCTTCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
Db      61 CCNTTATGHTGNGAGAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 120

Qy      248 CCTATGAGATGAGGAAATTTACACACTCTCTCTTATATGAGCCAGTGAATACAGTCCC 307
Db      121 CCNTATGAGATGAGGAAATTTACACACTCTCTCTTATATGAGCCAGTGAATACAGTCCC 180

Qy      308 AGTTACCTGAGGAAATTTACACTGACAGAGGTTACCTTGATCCCTGATTTCTAAT 367
Db      181 MSNTATCCGNGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240

Qy      368 TCTCTGATTTCCCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 427
Db      241 MSNCCNGNTTTCNTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300

Qy      428 GTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 487
Db      301 GTNCCNCCNTTNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 360

Qy      488 GCTGACAGACCCGCTGCCCCACCTATTGACAGCTGAGCTGAGCTGAGCTGAGCTGAG 547
Db      361 GNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 420

Qy      548 GCCACACTGTGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 607
Db      421 GCNACNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 480

Qy      608 GAGGACCTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 667
Db      481 GARGNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 540

Qy      668 GAGGACCTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 727
Db      541 GARGNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 600

Qy      728 GCCAAGCTGCTGCCCGGAGAACTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 784
Db      601 GCNARCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 657

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## RESULT 3

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US-08-728-323A-1/C
; Sequence 1, Application US/08728323A
; Patent No. 5948676
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohanzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
; TITLE OF INVENTION: Encoding Same And Uses Thereof
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-391-0525
TELEFAX: 212-278-0400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3489
US-08-728-323A-1

Query Match      12.0%; Score 121.2; DB 2; Length 3489;
Best Local Similarity 58.7%; Pred. No. 8.9e-20;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 413 GCTACTCAGTGAATGTTCTCTCCCTCCCTAGAGGGGTTCCCGTTGTCCTCTTCA 472
DB 2188 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2129
QY 473 AGGTTTTTTCAGCAGCTGACAGACCCGCTGCCCTATTTGACGTGAGCTGTGCA 532
DB 2128 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2069
QY 533 GCTGCACTCTTACAGCAGCAGCTGTAGACGTAGAGCTGTGAGAGGGCCCTGTGCA 592
DB 2068 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2009
QY 593 GCTGAGCTGTGACAGAGGACCTGTGAGCTGAGCTGAGCTGTGAGAGGACCTGTGCA 652
DB 2008 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1949
QY 653 GCTGAGCTGTGACAGAGGACCTGTGAGCTGAGCTGAGCTGAGAGGACCTGTGCA 712
DB 1948 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1889
QY 713 GCTGAGCTGTGACAGCAGCAGCTGTGAGCTGAGCTGAGCTGAGAGGACCTGTGCA 770
DB 1888 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1831

```

RESULT 4  
US-09-298-568-1/c

```

Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballesteras, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3489

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TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

Query Match      12.0%; Score 121.2; DB 4; Length 3489;
Best Local Similarity 58.7%; Pred. No. 8.9e-20;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 413 GCTACTCAGTGAATGTTCTCTCCCTCCCTAGAGGGGTTCCCGTTGTCCTCTTCA 472
DB 2188 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2129
QY 473 AGGTTTTTTCAGCAGCTGACAGACCCGCTGCCCTATTTGACGTGAGCTGTGCA 532
DB 2128 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2069
QY 533 GCTGCACTCTTACAGCAGCAGCTGTAGACGTAGAGCTGTGAGAGGGCCCTGTGCA 592
DB 2068 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2009
QY 593 GCTGAGCTGTGACAGAGGACCTGTGAGCTGAGCTGAGCTGAGAGGACCTGTGCA 652
DB 2008 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1949
QY 653 GCTGAGCTGTGACAGGACCTGTGAGCTGAGCTGAGCTGAGAGGACCTGTGCA 712
DB 1948 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1889
QY 713 GCTGAGCTGTGACAGCAGCAGCTGTGAGCTGAGCTGAGCTGAGAGGACCTGTGCA 770
DB 1888 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1831

```

RESULT 5  
US-09-410-399-1/c

```

Sequence 1, Application US/09410399
Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Colter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

Query Match      12.0%; Score 121.2; DB 4; Length 3489;
Best Local Similarity 58.7%; Pred. No. 8.9e-20;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 413 GCTACTCAGTGAATGTTCTCTCCCTCCCTAGAGGGGTTCCCGTTGTCCTCTTCA 472
DB 2188 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2129
QY 473 AGGTTTTTTCAGCAGCTGACAGACCCGCTGCCCTATTTGACGTGAGCTGTGCA 532
DB 2128 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2069
QY 533 GCTGCACTCTTACAGCAGCAGCTGTAGACGTAGAGCTGTGAGAGGGCCCTGTGCA 592
DB 2068 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2009
QY 593 GCTGAGCTGTGACAGAGGACCTGTGAGCTGAGCTGAGCTGAGAGGACCTGTGCA 652
DB 2008 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1949

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QY 653 GGTGAGCCTGCTGAGAGGACCTGTTGAGTGAGCCAGACCTGAGAGGACCTTACCA 712  
DB 1948 GCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCTGCTGCTGCTGCT 1889  
QY 713 GCTGAGCCTGCTGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770  
DB 1888 GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCT 1891

RESULT 6  
US-08-770-379-20

Sequence 20, Application US/08770379  
Patent No. 5449564  
GENERAL INFORMATION:  
APPLICANT: Chang, Yuan  
APPLICANT: Bohenzky, Roy A.  
APPLICANT: Russo, James J.  
APPLICANT: Edelman, Isidore S.  
APPLICANT: Moore, Patrick S.  
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED  
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,379  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 52442  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-770-379-20

Query Match 12.0%; Score 121.2; DB 2; Length 32207;  
Best Local Similarity 58.7%; Pred. No. 2.6e-19;  
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;  
QY 413 GCTACTCAGTTGAAAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 472  
DB 19809 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCAT 19868  
QY 473 AGGTTTTCAGCAGCTGAGACCCGCTGCCCACTATTGACGCTGAGCTGCTGCA 532  
DB 19869 CCTGCTGCTCTGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGCT 19928  
QY 533 GCTGACCTCTTAACAGCCACACCTGTAAGAGCTGAGCCGCTGAGAGGAGCCCTGTTGA 592  
DB 19929 GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCT 19988  
QY 593 GCTGAGCCTGCTGAGAGGACCTGTTGAGCTGAGCTGAGCTGCTGAGAGGACCTGTTGA 652  
DB 19989 GCTCATCTGCTGCTGCTCATCTCTGCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCT 20048

QY 653 GGTGAGCCTGCTGAGAGGACCTGTTGAGTGAGCCAGACCTGAGAGGACCTTACCA 712  
DB 20049 GCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCT 20108  
QY 713 GCTGAGCCTGCTGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770  
DB 20109 GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCT 20166

RESULT 7  
US-08-757-669A-20

Sequence 20, Application US/08757669A  
Patent No. 6183751  
GENERAL INFORMATION:  
APPLICANT: Chang, Yuan  
APPLICANT: Bohenzky, Roy A.  
APPLICANT: Russo, James J.  
APPLICANT: Edelman, Isidore S.  
APPLICANT: Moore, Patrick S.  
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS  
TITLE OF INVENTION: SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,669A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45185-F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-669A-20

Query Match 12.0%; Score 121.2; DB 3; Length 32207;  
Best Local Similarity 58.7%; Pred. No. 2.6e-19;  
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;  
QY 413 GCTACTCAGTTGAAAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 472  
DB 19809 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCAT 19868  
QY 473 AGGTTTTCAGCAGCTGAGACCCGCTGCCCACTATTGACGCTGAGCTGCTGCA 532  
DB 19869 CCTGCTGCTCTGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGCT 19928  
QY 533 GCTGACCTCTTAACAGCCACACCTGTAAGAGCTGAGCCGCTGAGAGGAGCCCTGTTGA 592  
DB 19929 GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCT 19988  
QY 593 GCTGAGCCTGCTGAGAGGACCTGTTGAGCTGAGCTGAGCTGCTGAGAGGACCTGTTGA 652



QY 526 TGTCTGAGCTGACCTCTTACAGCCACACCTGTAGAGCTGCTGCTGAGGGGCC 585  
DB 523 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582  
QY 586 TGTTCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645  
DB 583 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642  
QY 646 TGTTCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705  
DB 643 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702  
QY 706 TTTACAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729  
DB 703 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726

## RESULT 11

US-09-181-585-2  
Sequence 2, Application US/09181585  
Patent No. 6524791  
GENERAL INFORMATION:  
APPLICANT: Rannum, Laura P. W.  
APPLICANT: Koob, Michael  
TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION  
FILE REFERENCE: 11000900101  
CURRENT APPLICATION NUMBER: US/09/181,585  
CURRENT FILING DATE: 1998-10-28  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1471  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cDNA  
US-09-181-585-2

Query Match 9.9%; Score 100; DB 4; Length 1471;  
Best Local Similarity 56.8%; Pred. No. 7.8e-15;  
Matches 184; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 406 TCCCTTAGCTACTGAGTTGAATGTTCTCTCCCTCTAGGGGTTCCCGTTGTCCC 465  
DB 1025 TTCTTGGCTAGACCTGGGCTCTCATGTAGAAAACCTGCTTACTACTACTAC 1084  
QY 466 TCCCTTCAAGGTTTTTTCAGAGCTGAGAGCCCGCTGCCACCTATTGAGCTGAGCC 525  
DB 1085 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAC 1144  
QY 526 TGTTCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585  
DB 1145 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204  
QY 586 TGTTCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645  
DB 1205 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264  
QY 646 TGTTCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705  
DB 1265 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324  
QY 706 TTTACAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729  
DB 1325 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1348

RESULT 12  
US-09-253-691-3/c  
Sequence 3, Application US/09253691  
Patent No. 6124100

GENERAL INFORMATION:  
APPLICANT: Dong Kyu JIN  
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases  
FILE REFERENCE: 1942/36  
CURRENT APPLICATION NUMBER: US/09/253,691  
CURRENT FILING DATE: 1999-02-22  
EARLIER APPLICATION NUMBER: KR 98-6,278  
EARLIER FILING DATE: 1996-02-26  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: WordPerfect 6.1/Windows  
SEQ ID NO 3  
LENGTH: 397  
TYPE: DNA  
ORGANISM: human  
US-09-253-691-3

Query Match 9.3%; Score 93.6; DB 3; Length 397;  
Best Local Similarity 62.3%; Pred. No. 1.5e-13;  
Matches 147; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 481 TTTACAGCTGAGCAGCCCGCTGCCACCTATTGACAGCTGAGCTGCTGCTGAC 540  
DB 354 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 295  
QY 541 TTTACAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
DB 294 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235  
QY 601 TGTTCAGAGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
DB 234 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 175  
QY 661 TGTTCAGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716  
DB 174 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 119

## RESULT 13

5273901-6/c  
Patent No. 5273901  
APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON, SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.; AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.  
TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS  
SPOROZITE 21.5 KB ANTIGEN, AC-68  
NUMBER OF SEQUENCES: 11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/581,693  
FILING DATE: 12-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 215,162  
FILING DATE: 05-JUL-1988  
APPLICATION NUMBER: 746,520  
FILING DATE: 19-JUN-1985  
APPLICATION NUMBER: 627,811  
FILING DATE: 05-JUL-1984  
SEQ ID NO: 6  
LENGTH: 543  
5273901-6

Query Match 9.1%; Score 92; DB 6; Length 543;  
Best Local Similarity 54.4%; Pred. No. 4.2e-13;  
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 430 TGTCTCTCCCTCTGAGGGGTTTCCGTTTGTCTCTCTTCAAGGTTTTCAGAGC 489  
DB 354 TGTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 295  
QY 490 TGCAGACCCGCTGCGCCCACTATTGAGCTGAGCTGCTGCTGAGCTGACCTTTACAGC 549  
DB 294 TGTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235



Wed Jan 21 09:54:18 2004

us-09-923-236-1.rni

Page 8

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Job time : 92 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

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(without alignments)  
9063.677 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Published Applications NA:\*

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- 12: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1008	100.0	1008	10	US-09-922-469-1
4	981.6	97.4	1325	11	US-09-746-783-105
5	896.4	88.9	959	13	US-10-231-417-41
6	460	45.6	657	9	US-09-922-480-3
7	460	45.6	657	9	US-09-923-236-3
8	460	45.6	657	9	US-09-922-469-3
9	121.2	12.0	3489	13	US-10-294-804-1
10	100	9.9	1037	12	US-10-373-667-3
11	100	9.9	1159	12	US-10-373-667-1
12	100	9.9	1471	12	US-10-373-667-2
13	98.2	9.7	2108	10	US-09-962-832-225
14	92.4	9.2	1101	9	US-09-874-062-2
15	89.2	8.8	2183	12	US-10-104-047-1064

16	87.6	8.7	1101	9	US-09-874-062-2	Sequence 2, Appl1
17	85.2	8.5	1926	13	US-10-294-804-3	Sequence 3, Appl1
18	85.2	8.5	8705	15	US-10-291-230-14	Sequence 14, Appl1
19	85.2	8.5	8705	15	US-10-291-249-14	Sequence 14, Appl1
20	85.2	8.5	9600	13	US-10-278-751-1	Sequence 1, Appl1
21	85.2	8.5	10233	13	US-10-050-898-283	Sequence 283, App
22	85.2	8.5	10285	13	US-10-050-902-283	Sequence 283, App
23	84	8.3	1037	12	US-10-373-667-3	Sequence 3, Appl1
24	84	8.3	1159	12	US-10-373-667-1	Sequence 1, Appl1
25	84	8.3	1471	12	US-10-373-667-2	Sequence 2, Appl1
26	83.6	8.3	477	13	US-10-357-322-1	Sequence 1, Appl1
27	83	8.2	2183	12	US-10-104-047-1064	Sequence 1064, Ap
28	78.2	7.8	16442	12	US-10-374-077-208	Sequence 208, App
29	77.8	7.7	422	10	US-09-738-973-337	Sequence 337, App
30	77.8	7.7	422	10	US-09-854-133-337	Sequence 337, App
31	77.8	7.7	422	15	US-10-144-649A-337	Sequence 337, App
32	75	7.4	14859	12	US-10-051-874-55	Sequence 55, Appl
33	73.4	7.3	9369	13	US-10-200-562-190	Sequence 190, App
34	73.4	7.3	9369	13	US-10-237-551-190	Sequence 190, App
35	73.4	7.3	9369	13	US-10-237-551-247	Sequence 247, App
36	73.4	7.3	154746	13	US-09-827-688-8	Sequence 8, Appl1
37	73.2	7.2	14859	12	US-10-051-874-55	Sequence 55, Appl
38	72.6	7.2	1388	12	US-10-264-049-518	Sequence 518, App
39	72.2	7.2	469	13	US-10-029-386-20613	Sequence 20613, A
40	72.2	7.2	5379	15	US-10-128-714-5305	Sequence 5305, Ap
41	71.8	7.1	2404	12	US-10-104-047-1740	Sequence 1740, Ap
42	71.8	7.1	3439	12	US-10-161-927-53	Sequence 53, Appl
43	71.6	7.1	628	13	US-10-029-386-22859	Sequence 22859, A
44	71.6	7.1	1008	9	US-09-922-480-1	Sequence 1, Appl1
45	71.6	7.1	1008	9	US-09-923-236-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-922-480-1  
Sequence 1, Application US/09922480  
Patent No. US20020081701A1  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: SECRETED SALIVARY ZS163 POLYPEPTIDE  
FILE REFERENCE: 97-71  
CURRENT APPLICATION NUMBER: US/09/922,480  
CURRENT FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/124,820  
PRIOR FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PasteSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 1008  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (128)...(784)  
US-09-922-480-1

Query Match 100.0%; Score 1008; DB 9; Length 1008;  
Best Local Similarity 100.0%; Pred. No. 1, ie-236;  
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACAGACTAAAAAGCCATGATCTTCTCTCTAAAGAGAAAAATTAATT 60  
1 AGACAGACTAAAAAGCCATGATCTTCTCTCTCTAAAGAGAAAAATTAATT 60  
DB 61 TAAATATCATGCGTATTTCTTAAACAATTAATGTTAATATCATAGGCTC 120  
61 TAAATATCATGCGTATTTCTTAAACAATTAATGTTAATATCATAGGCTC 120  
QY 121 AATCAATGAAGCTTCCTCTGGGCTGATGATGTTGCTTTGCAAGAGAG 180  
|||||

Db 121 AATCAAAATGAAGCTTCTCTTGGGCTGATGTGATGTGCTTTTGAAGAAG 180  
Qy 181 ACGTTTCCCTTCATTTGGTGAAGATGACATAGATGTGACCCACTTCATCTT 240  
Db 181 ACGTTTCCCTTCATTTGGTGAAGATGACATAGATGTGACCCACTTCATCTT 240  
Qy 241 GAATATCTCTTATGAGATGAGAAATTTACACCTCTCTTTATATGAGGAAATAC 300  
Db 241 GAATATCTCTTATGAGATGAGAAATTTACACCTCTCTTTATATGAGGAAATAC 300  
Qy 301 AGTCCCAAGTACCTCTGGAATATCTTACATGACACAGGTTACCTCTGATCTCTGAT 360  
Db 301 AGTCCCAAGTACCTCTGGAATATCTTACATGACACAGGTTACCTCTGATCTCTGAT 360  
Qy 361 TCTAATCTTCTGATTTCCCTGATGTGATGATGATGATGATGATGATGATGATGAT 420  
Db 361 TCTAATCTTCTGATTTCCCTGATGTGATGATGATGATGATGATGATGATGATGAT 420  
Qy 421 GTTGAATGTTCT 480  
Db 421 GTTGAATGTTCT 480  
Qy 481 TTCAAGACGTGACGACCCGCTGACCCGCTGACCTTATGACGCTGACGCTGACGCTGAC 540  
Db 481 TTCAAGACGTGACGACCCGCTGACCCGCTGACCTTATGACGCTGACGCTGACGCTGAC 540  
Qy 541 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 600  
Db 541 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 600  
Qy 601 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 660  
Db 601 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 660  
Qy 661 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Db 661 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Qy 721 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 780  
Db 721 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 780  
Qy 781 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 840  
Db 781 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 840  
Qy 841 GAAATCTACAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
Db 841 GAAATCTACAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
Qy 901 ATTATCTACAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960  
Db 901 ATTATCTACAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960  
Qy 961 AAAAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008  
Db 961 AAAAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008

RESULT 2  
US-09-923-236-1

; Sequence 1, Application US/09923236  
; Patent No. US20020090677A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Adler, David A.  
; TITLE OF INVENTION: SECRETED SALIVARY ZS1G63 POLYPEPTIDE  
; FILE REFERENCE: 97-71  
; CURRENT APPLICATION NUMBER: US/09/923,236  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/124,820  
; PRIOR FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1008  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (128)...(784)  
US-09-923-236-1  
Query Match 100.0%; Score 1008; DB 9; Length 1008;  
Best Local Similarity 100.0%; Pred. No. 1.1e-236;  
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGACGACTTAAAGGATGATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60  
Db 1 AGACGACTTAAAGGATGATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60  
Qy 61 TAAATATCATTTGGGATTTTCTTAAACATTAATTAATTAATTAATTAATTAATTAATTAAT 120  
Db 61 TAAATATCATTTGGGATTTTCTTAAACATTAATTAATTAATTAATTAATTAATTAATTAAT 120  
Qy 121 AATCAAAATGAAGCTTCTCTTGGGCTGATGTGATGTGATGTGATGTGATGTGATGTGAT 180  
Db 121 AATCAAAATGAAGCTTCTCTTGGGCTGATGTGATGTGATGTGATGTGATGTGATGTGAT 180  
Qy 181 ACGTTTCCCTTCATTTGGTGAAGATGACATAGATGTGACCCACTTCATCTTCT 240  
Db 181 ACGTTTCCCTTCATTTGGTGAAGATGACATAGATGTGACCCACTTCATCTTCT 240  
Qy 241 GAATATCTCTTATGAGATGAGAAATTTACACCTCTCTTTATATGAGGAAATAC 300  
Db 241 GAATATCTCTTATGAGATGAGAAATTTACACCTCTCTTTATATGAGGAAATAC 300  
Qy 301 AGTCCCAAGTACCTCTGGAATATCTTACATGACACAGGTTACCTCTGATCTCTGAT 360  
Db 301 AGTCCCAAGTACCTCTGGAATATCTTACATGACACAGGTTACCTCTGATCTCTGAT 360  
Qy 361 TCTAATCTTCTGATTTCCCTGATGTGATGATGATGATGATGATGATGATGATGAT 420  
Db 361 TCTAATCTTCTGATTTCCCTGATGTGATGATGATGATGATGATGATGATGATGAT 420  
Qy 421 GTTGAATGTTCT 480  
Db 421 GTTGAATGTTCT 480  
Qy 481 TTCAAGACGTGACGACCCGCTGACCCGCTGACCTTATGACGCTGACGCTGACGCTGAC 540  
Db 481 TTCAAGACGTGACGACCCGCTGACCCGCTGACCTTATGACGCTGACGCTGACGCTGAC 540  
Qy 541 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 600  
Db 541 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 600  
Qy 601 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 660  
Db 601 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 660  
Qy 661 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Db 661 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Qy 721 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 780  
Db 721 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 780  
Qy 781 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 840  
Db 781 TCTTACAGCAGCAGCTGTGAGAGCTGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 840  
Qy 841 GAAATCTACAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
Db 841 GAAATCTACAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900





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? INFORMATION FOR SEQ ID NO: 105:
?     SEQUENCE CHARACTERISTICS:
?         LENGTH: 1325 base pairs
?         TYPE: nucleic acid
?         STRANDEDNESS: double
?         TOPOLOGY: linear
?     MOLECULE TYPE: cDNA
?     SEQUENCE DESCRIPTION: SEQ ID NO: 105
? 5'-GG-746-783-105

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Query Match 97.4%;	Score 981.6;	DB 11;	Length 1325;
Best Local Similarity 99.5%;	Pred. No. 3.9e+230;		
Matches 995;	Conservative 0;	Mismatches 4;	Indels 1;
			Gaps 1.

Qy	10	AAAAAGCCATGATATCTTGGTTCTCTCTAAAGAAAGAAAATATATTTAAAAATAC	69
Db	9	AAAAAGCCATGATATCTTGGTTCTCTCTAAAGAAAGAAAATATATTTAAAAATAC	68
Qy	70	ATTGCGATTTTCTAAAACAATPAATTTATAGTTAAATATTCAAGGGTCATCAAAAT	129
Db	69	ATTGCGATTTTCTAAAACAATPAATTTATAGTTAAATATTCAAGGGTCATCAAAAT	128
Qy	130	GAAGCTTTCCTTGGAGCCGCACTGTATAGTGTGCTTTTGCAAGAAAGACGGTCCC	189
Db	129	GAAGCTTTCCTTGGAGCCGCACTGTATAGTGTGCTTTTGCAAGAAAGACGGTCCC	188
Qy	190	CTTCATTGTGAGATGACATAGACGATGGTCACCACCTTCATCCATCTGAAATATTC	249
Db	189	CTTCATTGTGAGATGACATAGACGATGGTCACCACCTTCATCCATCTGAAATATTC	248
Qy	250	TTATGCGATACGGAAATTTACACCTCTCTTTATATAGCCACGAAATACAGTCCCAG	309
Db	249	TTATGCGATACGGAAATTTACACCTCTCTTTATATAGCCACGAAATACAGTCCCAG	308
Qy	310	TTACCCGTGGAAATACCTTACATGACACAGAGGTTACCTTCGATCCCTGGAATTCATCTTC	369
Db	309	TTACCCGTGGAAATACCTTACATGACACAGAGGTTACCTTCGATCCCTGGAATTCATCTTC	368
Qy	370	TCTCGAATTCCTTATGTCTATACATCCGAGGTTTCCCTTACGTACTCACTGAAATGT	429
Db	369	TCTCGAATTCCTTATGTCTATACATCCGAGGTTTCCCTTACGTACTCACTGAAATGT	428
Qy	430	TCTCCCTCTCCCTCTAAGGGGTTTCCCGTTGTCCTCTCAAGGTTTTTTTACAGAGC	489
Db	429	TCTCCCTCTCCCTCTAAGGGGTTTCCCGTTGTCCTCTCAAGGTTTTTTTACAGAGC	488
Qy	490	TGCAGCAACCGCATGCCCACTAATGACAGCTGAGCCTGTGACGCTCTTAACAGC	549
Db	489	TGCAGCAACCGCATGCCCACTAATGACAGCTGAGCCTGTGACGCTCTTAACATC	548
Qy	550	CACACCTGTAGAGCTGAGCCTGTGTGCAAGGGGCCCTGTGTGACGTGACCTGTGTGAGA	609
Db	549	CACACCTGTAGAGCTGAGCCTGTGTGCAAGGGGCCCTGTGTGACGTGACCTGTGTGAGA	608
Qy	610	GGCACCCTGTGAGAGCTGAGCCTGTGTGCAAGGCACTGTGTGACGTGTGTGAGAGA	669
Db	609	GGCACCCTGTGAGAGCTGAGCCTGTGTGCAAGGCACTGTGTGACGTGTGTGAGAGA	668
Qy	670	GGCACCCTGTGAGAGGAGGAGCCTGACAGAGGAACCTTACCAAGCTGAGCCTGTGTACAGC	729
Db	669	GGCACCCTGTGAGAGGAGGAGCCTGACAGAGGAACCTTACCAAGCTGAGCCTGTGTACAGC	728
Qy	730	CAGAGCCGTGCCCCCAAGAACTCAACCTTCTCCCTCTGTAAACAGGCAATTCAGTAAA	789
Db	729	CAGAGCCGTGCCCCCAAGAACTCAACCTTCTCCCTCTGTAAACAGGCAATTCAGTAAA	788
Qy	790	TTCTCTAGAGAGTACCATGAGGTTCAATTTCTATCTGATGACAAATATAGAAATCTAC	849
Db	789	TTCTCTAGAGAGTACCATGAGGTTCAATTTCTATCTGATGACAAATATAGAAATCTAC	848
Qy	850	AAAAAGTTTCTTTCTTTTCCAAAAGCTAATTTCAATCTGTGTATTCAAGATTAATCATCTC	909
Db	849	AAAAAGTTTCTTTCTTTTCCAAAAGCTAATTTCAATCTGTGTATTCAAGATTAATCATCTC	908

[illegible]

RESULT 5  
US-10-231-417-41

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Sequence 41, Application US/10231417
Publication No. US20030176681A1
GENERAL INFORMATION:
APPLICANT: Peng et al
TITLE OF INVENTION: 148 Human Secreted Proteins
FILE REFERENCE: P2019P1
CURRENT APPLICATION NUMBER: US/10/731,417
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US/09/296,622
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 619
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 959
TYPE: DNA
ORGANISM: Homo sapiens
US-10-231-417-41

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	Query Match	88.9%	Score 896.4	DB 13	Length 959	
	Best Local Similarity	98.8%	Pred. No. 2.5e-209			
Matches	923	Conservative	1	Mismatches	7	Indels
						Gaps
						2
QY	75	GTATTTCTTAAACAGATAAATTTA	TAGTGTTAATATTCATGAGGGTCATCAAAAATGAAGC	134		
DB	12	GTATTTCTTAAACAGATAAATTTA	TAGTGTTAATATTCATGAGGGTCATCAAAAATGAAGC	71		
QY	135	TTCTCCCTTTGGGCCCTGCATTGTATGTGTGCTTTTGGCAAGNAGAAGCGTTCCCTTCA	194			
DB	72	TTCTCCCTTTGGGCCCTGCATTGTATGTGTGCTTTTGGCAAGNAGAAGCGTTCCCTTCA	131			
QY	195	TTGGTAGAGATGACAAATGACAGATGGTCAACCACACTTACATCTCTGTAATATTCTCTTAATG	254			
DB	132	TTGGTAGAGATGACAAATGACAGATGGTCAACCACACTTACATCTCTGTAATATTCTCTTAATG	191			
QY	255	GCATACGGAAATTATACCACTCTCTCTTTATATATGCGCCAGTAATPACAGTCCCCAGTTACC	314			
DB	192	GCATACGGAAATTATACCACTCTCTCTTTATATATGCGCCAGTAATPACAGTCCCCAGTTACC	251			
QY	315	CTGGGAATACCTAACACATGACACAGGGTTACCTTGATCCCTGGATTTCTAATTCTCTCTG	374			
DB	252	CTGGGAATACCTAACACATGACACAGGGTTACCTTGATCCCTGGATTTCTAATTCTCTCTG	311			
QY	375	GATTCCCTCATATGTCTATCACATCCGTGGTTTTTCCCTTAGCTACTACAGTGAATGTTCTCTC	434			
DB	312	GATTCCCTCATATGTCTATCACATCCGTGGTTTTTCCCTTAGCTACTACAGTGAATGTTCTCTC	371			
QY	435	CTTCCCTCTCTAGAGGGTTTTCCCGTTTGTCCCTCCTTCAAAGTTTTTTTACAGAGCTGCAG	494			
DB	372	CTTCCCTCTCTAGAGGGTTTTCCCGTTTGTCCCTCCTTCAAAGTTTTTTTACAGAGCTGCAG	431			
QY	495	CACCCGCGGCCCACTATTGACAGTGAAGCTGTGGCGAGCTGCAGCACTTTACAGCCACAC	554			
DB	432	CACCCGCGGCCCACTATTGACAGTGAAGCTGTGGCGAGCTGCAGCACTTTACAGCCACAC	491			
QY	555	CTGTAGCAGCTGAGCTGTGCTGCAGAGGGGCCCTGTGTGACGTGAGCCTGCTG--CAGAGGC	612			
DB	492	CTGTAGCAGCTGAGCTGTGCTGCAGAGGGGCCCTGTGTGACGTGAGCCTGCTG--CAGAGGC	551			
QY	613	ACCTGTTTBGAGC-TBAGCTGTGCTGCAGAGGCACTGTGTGACGTGAGCTGTGCTGTGAGAGG	671			
DB	552	ACCTGTTTBGAGCTGTGAGCTGTGCTGCAGAGGCACTGTGTGACGTGAGCTGTGCTGTGAGAGG	611			

Qy 672 CACCTGTTGAGTGAAGCAGCTGACAGAAACCTTCCAGCTGAGCTGCTACAGCA 731  
Db 612 CACCTGTTGAGTGAAGCAGCTGACAGAAACCTTCCAGCTGAGCTGCTACAGCA 671  
Qy 732 AGCCTGCTGCCCCAGAACTCACCCTTCTCCTCTCTTGAACAGCAATCAGTGAAT 791  
Db 672 AGCCTGCTGCCCCAGAACTCACCCTTCTCCTCTCTTGAACAGCAATCAGTGAAT 731  
Qy 792 CTCTAGAAAGTACCACTGCTTCACTTCTATCTGATGACAGAAATAGTGAATCTCA 851  
Db 732 CTCTAGAAAGTACCACTGCTTCACTTCTATCTGATGACAGAAATAGTGAATCTCA 791  
Qy 852 AAGTTTCTTCTTCTTCCAAAGACATCTTCTGTTGATGACAGATCTTCTTCTCAC 911  
Db 792 AAGTTTCTTCTTCTTCCAAAGACATCTTCTGTTGATGACAGATCTTCTTCTCAC 851  
Qy 912 TACATTTGATTTGTTGTGTGTTTCTTCTGACCTTATTTATTTGAAAAACATTTGA 971  
Db 852 TACATTTGATTTGTTGTGTGTTTCTTCTGACCTTATTTATTTGAAAAACATTTGA 911  
Qy 972 TAAATTAATAATAATAATAGATTAATTAGACCA 1005  
Db 912 TAAATTAATAATAATAATAGATTAATTAGACCA 945

# RESULT 6

US-09-922-480-3  
; Sequence 3, Application US/09922480  
; Patent No. US20020081701A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Adler, David A.  
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE  
; FILE REFERENCE: 97-71  
; CURRENT APPLICATION NUMBER: US/09/922,480  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/124,820  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Degenerate polynucleotide sequence for zsig63  
; NAME/KEY: misc\_feature  
; LOCATION: (1)-(657)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-922-480-3

Query Match 45.6%; Score 460; DB 9; Length 657;  
Best Local Similarity 61.0%; Pred. No. 1.9e-102;  
Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

Qy 128 ATGAAGCTTCTCTTGGGCGCTGATGTATGTGCTTTTGGCAAGAGACGGTTTC 187  
Db 1 ATGAARTYNTYNTYNTGGGCGCTGATGTATGTGCTTTTGGCAAGAGAGMGNNTTY 60  
Qy 188 CCGCTTATTTGTTGAGATGACATGATGTCACCACTTCACTCTCTGAAATTT 247  
Db 61 CCNTTYATHGGNGAGAYGAAYAAAGAYAGGNCAYCCNYTNCAACWMSNTYTAAYATH 120  
Qy 248 CCTTATGCGATACGGAATTTACCACTCTCTTATTTAGCCGAGTAAATACGCTCCC 307  
Db 121 CCNTAYGSAATHMGNAAAYTTCNCNCNCNTNTATYATMGNCCNGTAAAYACNGTNCN 180  
Qy 308 AGTTACCTGGGAATACCTTACACTGACACAGGGTTACCTTGATCCCTGATTTCTA 367  
Db 181 WSNATYCCNGGNAAYACNTAYACNGAYACNGGNTTNCWMSNTAYCCNTGATHTYTA 240  
Qy 368 TCTCTGATTCCTCTATGTCTATGACATCCCTGCTTTTCCCTAGCTACTCAGTTGAT 427

Db 241 MSNCCNGGNTTYCCNTATYAGNTATYCAVATHMGNAGNTTYCCNTYNGNACGATTAAY 300  
Qy 428 GTTCTCTCTCTCCTCTAGGGGTTTCCGTTTGTCCCTCTTCAAGTTTTCAGCA 487  
Db 301 GTNCCNCNTYNTCCNCNMGGGNTTYCCNTYGTNCNCNCNMNTNTYTTYSNGCN 360  
Qy 488 GCTGACACCCGCTGCCCCACCTATTTGACCTGAGCTGCTGACCTGACCTCTTACA 547  
Db 361 GCNCCNCNCNCNCNCNCNCNATHGNCNGARCCNCCNCCNCCNCCNYTAACN 420  
Qy 548 GCCACACTGTAGCAGCTGAGCTGTGACAGGGGCCCTGTGAGCTGAGCTGTGCA 607  
Db 421 GCNACNCNCNTYNGNCCNGARCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 480  
Qy 608 GAGGCACTGTTGAGAGCTGAGCTGTGACAGGCACTGTTGAGCTGAGCTGTGCA 667  
Db 481 GARGCNCNCTYNGNCCNGARCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 540  
Qy 668 GAGGCACTGTTGAGAGCTGAGCTGTGACAGGCACTTACAGCTGAGCTGTGCA 727  
Db 541 GARGCNCNCTYNGNCCNGARCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 600  
Qy 728 GCCAAGCTGCTGCCCCAGAACTCACCCTTCTCTCTTGAACAGCAATCAG 784  
Db 601 GCNARCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 657

# RESULT 7

US-09-923-236-3  
; Sequence 3, Application US/09923236  
; Patent No. US20020090677A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Adler, David A.  
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE  
; FILE REFERENCE: 97-71  
; CURRENT APPLICATION NUMBER: US/09/923,236  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/124,820  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Degenerate polynucleotide sequence for zsig63  
; NAME/KEY: misc\_feature  
; LOCATION: (1)-(657)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-923-236-3

Query Match 45.6%; Score 460; DB 9; Length 657;  
Best Local Similarity 61.0%; Pred. No. 1.9e-102;  
Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

Qy 128 ATGAAGCTTCTCTTGGGCGCTGATGTATGTGCTTTTGGCAAGAGACGGTTTC 187  
Db 1 ATGAARTYNTYNTYNTGGGCGCTGATGTATGTGCTTTTGGCAAGAGAGMGNNTTY 60  
Qy 188 CCGCTTATTTGTTGAGATGACATGATGTCACCACTTCACTCTCTGAAATTT 247  
Db 61 CCNTTYATHGGNGAGAYGAAYAAAGAYAGGNCAYCCNYTNCAACWMSYTTAAAYATH 120  
Qy 248 CCTTATGCGATACGGAATTTACCACTCTCTTATTTAGCCGAGTAAATACGCTCCC 307  
Db 121 CCNTAYGSAATHMGNAAAYTTCNCNCNCNTNTATYATMGNCCNGTAAAYACNGTNCN 180  
Qy 308 AGTTACCTGGGAATACCTTACACTGACACAGGGTTACCTTGATCCCTGATTTCTA 367  
Db 181 WSNATYCCNGGNAAYACNTAYACNGAYACNGGNTTNCWMSNTAYCCNTGATHTYTA 240

Oy 368 CTTCTGGAATTCCTCCATATCATACATCCGGATTTTCCCTAGTACTAGATGAAT 4227  
 Db 241 MSNCNGSNITTYCCNTATYGTNTAYCAATHTMGAGTTTCNTTNGCNACNCAATMAAY 3000  
 Oy 428 GTTCTCTCTCTCCCTCTTAGGGGGTTCCTCGTTTGTCTCTCTTCAAGATTTTTAGCA 487  
 Db 301 GTNCNCNCNYTNCNCNCNMGNGNTTTYCCNTTYGTNCNCNCNMSNMGNNTTTYTWSNGCN 3606  
 Oy 488 GCTGAGACACCCGCTGGCCCACTATTTGCACTGAGCCTGTCTGACGTGACCTCTTACA 547  
 Db 361 GGNCGNCGNCNCGNCGNCNCNCMAATHGNCNCGNCAACNCGNCGNCGNCCNYTNACN 420  
 Oy 548 GCCACACCTGTAGACAGCTGAGCCTGTGTGACGGGGCCCTGTGTGACGTGACCTGTGCA 607  
 Db 421 GCNACNCNCNTMGNCNCGNCAACNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 480  
 Oy 608 GAGGCACTGTGTGAGACTGAGCCTGTGTGACGAGGACACTGTGTGACGTGAGCCTGTGCA 667  
 Db 481 GARGCNCNCNTMGNCNCGNCAACNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 540  
 Oy 668 GAGGCACTGTGTGAGACTGAGCAGCTGTGACGAGGAACCTTACACAGCTGAGCCTGTGACA 727  
 Db 541 GARGCNCNCNTMGNGTNGARCCNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 600  
 Oy 728 GCCAAGCCGTGCGCCCAAGAACTCAACCTTTCCTCTTCAACAGGGAATTCAG 784  
 Db 601 GCNAAATCCNCGNCGNCGNCAACNCAATCCNWSNCCNWSNTTNGARCAAGCNAATYCAR 657

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RESULT 8
US-09-922-469-3
; Sequence 3, Application US/09922469
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZS1G63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,469
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate polynucleotide sequence for zsig63
; NAME/KEY: misc feature
; LOCATION: (1) ... (657)
; OTHER INFORMATION: n = A,T,C or G
US-09-922-469-3

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Query Match	45.6%	Score 460;	DB 10;	Length 657;
Best Local Similarity	61.0%	Pred. No. 1.9e-102;		
Matches 401;	Conservative 103;	Mismatches 153;	Indels 0;	Gaps 0

Qy	128	TTGAAGCTTCTCCCTTGGGCGTCAGATCTGATGTTGGCTTTGGCAAGAAACCGCTTC	187
Db	1	ATGAARVYNYNYNYTATGGCGNTGYAHHGNTGTGTNGCMTTGYGCMNGAARMNMCGATTY	60
Qy	188	CCCTTCATTTGGTGAAGATGACAATGACGATGGCGACCCACTTCATCATCTCTGAAATATT	247
Db	61	CCNTTYAATHGNGAAGAYGATYAAVGAIVGAGNCATCCNTTNCAYCCMNSNYTAAAYATH	120
Qy	248	CCCTTATGGCATACGGAATTTATCCACCTCTCTTATATTCGCCCAAGTATACAGTCCCC	307
Db	121	CCNTAIVGGNAATHMGNAAYTTTNCNCNCNCNTYNTATATATMGNCNGTNAAYACNGTNCN	180
Qy	308	AGTTACCTCGGAATATTACACTGACACAGGGTTACTCTTCGATCCCTGGATTTCTAACT	367

Db 131 MSNTAYCCNGGNAAYACTATAYACNGAYACNGSNTYNNCCMSYTAACNTGGAHTHYNNACN 240

QY 368 TCTCTGATYTTCCCTATGTCATACATCCGTGGTGTTCCTTAGCTACTCAGTTGAAT 427

Db 241 MSNCCNGSNTTYCCNTAYGTNTAYACAYATHMNGSNTTYCCNYTNGCNAKCNCARYNMAAY 300

QY 428 GTTCTCCTCTCCCTCTTACGGGGGTTTCCCGTTCCTCCCTCTTCAAGGTTTTCACGA 487

Db 301 GTNCCNCCNYTNCNCNCMMNGSNTTYCCNTTYGTNCCNCCMSNMGNNTTYTTCWSNGCN 360

QY 488 GCTGACGACCCGCGTCCGCCACCTATTTGACGCTGAGCCTGTGACGCTCAGCTCACTCTTACA 547

Db 361 GGNCGNCGNCCNGCNGCNCNCNNAITHGNGCNGARCCNGCNGCNGCNGCNCNTYNACN 420

QY 548 GCCACACCTGTAGACAGCTGAGCCTCTGTGACGGGGCCCCCTGTTGACGTAGCCTGTGTGA 607

Db 421 GCMNCNCNGTNGCNGCNGARCCNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 480

QY 608 GAGGACCTGTGTGAGCTGAGCCTGTCTGTGACGACCTGTGTCAGCTGTCTGTGA 667

Db 481 GARGCNCNGTNGCNGCNGARCCNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 540

QY 668 GAGGACCTGTGTGAGCTGAGCCTGTCTGTGACGACCTGTGTCAGCTGTCTGTGA 727

Db 541 GARGCNCNGTNGGNGTNGARCCNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 600

QY 728 GCCAAGCCTGTGCCCCCAGAACTCAACCTTCTCTCTCTGTGAACGAGCAATATTCAG 784

Db 601 GCMAARCCNGCNGCNCNGARCCNCAAYCCMWSNCCMSYTTTGARCARCCNMAAYCAR 657

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RESULT 9
US-10-294-804-1/c
: Sequence 1, Application US/10294804
: Publication NO. US20030133948A1
: GENERAL INFORMATION:
: APPLICANT: Robertson, Erle S.
: APPLICANT: Cotter, Murray A.
: TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
: TITLE OF INVENTION: to Genomic Host DNA
: FILE REFERENCE: UM-03778
: CURRENT APPLICATION NUMBER: US/10/294,804
: CURRENT FILING DATE: 2002-11-14
: PRIORITY APPLICATION NUMBER: US/09/410,399
: PRIOR FILING DATE: 1999-10-01
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3489
: TYPE: DNA
: ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-294-804-1

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Query Match	12.0%;	Score 121.2;	DB 13;	Length 3489;
Best Local Similarity	58.7%;	Pred. No. 6.5e-19;		
Matches 210;	Conservative	0;	Mismatches 148;	Indels 0;
				Gaps 0;

QY	413	GCTACTAGTTGAAGTTCCTCTCTCTCCCTCCGAGGGATTTCCCGTTGTCCTCTTCA	472
Db	2188	GCTGCTATCCTGCTGCTGCTCTCATCTGCTGTGTCTCATCTGCTGCTCTGCTCAT	2122
QY	473	AGGTTTTTTTCAGCAGCTGACAGCACCCGCTGCCCCACCTATTGACGTGAGGCTGTGCA	532
Db	2128	CCTGCTGTCCTGCTCATCTGCTGCTCTGTCTATCTGCTGCTGCTCATCTGCTGCT	2065
QY	533	GCTGCACCTTTTACGCCACACTGTGACAGCTGAGCTGTCGACGGGGCCCTGTGCA	592
Db	2068	GCTCATCTGCTGCTGCTCATCTGCTGCTCTCATCTGCTGCTGCTCATCTGCTGCT	2005
QY	593	GCTGAGCTTGTGACAGGAGCACTGTGAACTGAGCCTGCTGACGAGAGCACTGTGCA	652
Db	2008	GCTATCTCTGCTGCTCATCTGCTGCTGTCTATCTGCTGCTGCTCATCTGCTGCT	1944





[illegible]

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Search completed: January 16, 2004, 10:30:01
Job time : 397 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: January 16, 2004, 07:13:18 : Search time 2130 Seconds  
(without alignments)  
11501.837 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008  
Sequence: 1 agacagactaaagacat.....tagataattagaccatgg 1008

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hrc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hrc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	703	69.7	703	2	HSM075873 Bx485686 Homo sapi
2	680.4	67.5	682	2	HSM076010 Bx485823 Homo sapi
3	677.4	67.2	742	14	CB957562 AGENCOURT
4	667	66.2	677	2	HSM075890 Bx485703 Homo sapi

5	655	65.0	669	2	HSM075629 Bx485442 Homo sapi
6	655	65.0	677	2	HSM076867 Bx486680 Homo sapi
7	654.6	64.9	675	2	HSM076755 Bx486688 Homo sapi
8	647	64.2	675	2	HSM076748 Bx486561 Homo sapi
9	641.4	63.6	665	2	HSM075590 Bx485403 Homo sapi
10	640.4	63.5	678	2	HSM077932 Bx487745 Homo sapi
11	633.4	62.8	647	2	HSM077857 Bx487670 Homo sapi
12	614.2	60.9	672	2	HSM074459 Bx484273 Homo sapi
13	605	60.0	658	2	HSM075827 Bx485640 Homo sapi
14	603.4	59.9	618	2	HSM074630 Bx484444 Homo sapi
15	585.4	58.1	610	2	HSM075337 Bx485150 Homo sapi
16	562	55.8	573	2	HSM076631 Bx486444 Homo sapi
17	549.4	54.5	572	2	HSM076126 Bx485939 Homo sapi
18	541.8	53.8	572	2	HSM074549 Bx484363 Homo sapi
19	519	51.5	531	2	HSM076965 Bx486778 Homo sapi
20	516.8	51.3	591	2	HSM076729 Bx486542 Homo sapi
21	490.6	48.7	542	2	HSM081001 Bx509214 Homo sapi
22	483.8	48.0	498	2	HSM076978 Bx486791 Homo sapi
23	483.8	48.0	503	2	HSM076402 Bx486215 Homo sapi
24	476	47.2	491	2	HSM076125 Bx485938 Homo sapi
25	467.8	46.4	483	2	HSM075308 Bx485121 Homo sapi
26	451	44.7	514	2	HSM075124 Bx484937 Homo sapi
27	433.6	43.0	449	2	HSM076457 Bx486270 Homo sapi
28	403.8	40.1	504	2	HSM076054 Bx485867 Homo sapi
29	394	39.1	405	2	HSM077483 Bx487296 Homo sapi
30	299	29.7	299	2	HSM077075 Bx486688 Homo sapi
31	258.2	25.6	437	2	HSM077573 Bx487286 Homo sapi
32	227	22.5	227	2	HSM074843 Bx484657 Homo sapi
33	215	21.3	747	14	CB958709 AGENCOURT
34	178.2	17.7	682	2	HSM075684 Bx485497 Homo sapi
35	153	15.2	1302	11	AK015291 BFA45627 UT-R-BTO-
36	133	13.2	499	10	BF544627 UT-R-BTO-
37	131.2	13.0	492	28	AQ133079 HS_2188_A
38	131	13.0	926	14	BY714849 BY714849
39	125.8	12.5	711	12	BM934267 UT-M-CG0P
40	109.6	10.9	700	14	CAS10498 UT-R-FU0-
41	109.6	10.9	754	14	CAS12401 UT-R-FU0-
42	109.6	10.9	756	14	CAS12995 UT-R-FU0-
43	108	10.7	594	14	CB584404 AMGNUTC:M
44	108	10.7	605	28	AZ640388 IM0502E21
45	108	10.7	718	28	AZ972907 2M0246M24

## ALIGNMENTS

RESULT 1  
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ID HSM075873 strand: RNA; EST: 703 BP.  
XX AC Bx485686;  
XX SV Bx485686.1  
XX DT 09-MAY-2003 (Rel. 75, Created)  
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)  
XX DE Homo sapiens mRNA; EST DKFZp686C15248\_r1 (from clone DKFZp686C15248)  
XX KW EST, expressed sequence tag.  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
XX RN [1]  
RP 1-703  
RA Ottenwelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B.,  
RA Amid C., Osanger A., Fobo G., Han W., Wiemann S.,  
RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.  
RL MRS, Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY  
XX

CC	This is the 5' sequence of the clone insert
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
CC	sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium available.
CC	No s1 sequence available.
CC	This clone (DKFZ686c15248) is available at the RZPD in Berlin.
CC	Please contact the RZPD; Ressourcenzentrum, Heubnerweg 6,
CC	14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX	
FH	Key
FH	Location/Qualifiers
FT	source
FT	1..703
FT	/db_xref="taxon:9606"
FT	/mol_type="mRNA"
FT	/organism="Homo sapiens"
FT	/clone="DKFZp686C15248"
FT	/clone_lib="686 (synonym: hicc3). Vector pSport1_Sfi; host DH10B; sites SfiI + SfiIb"
FT	/dev_stage="adult"
FT	/tissue_type="CDNA-collection"
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SQ	Sequence 703 BP; 158 A; 195 C; 151 G; 199 T; 0 other;
Query Match	69.7%; Score 703; DB 2; Length 703;
Best Local Similarity	100.0%; Pred. No. 1.le-103;
Matches 703; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	38 TCATAAAGAGAAAAATATATTATTTAAATAATACATTGCGATTTTCTAAACAATAAATTT
DB	1 TCTAAAAGAAGAAAAATATATTATTTAAATAATACATTGCGATTTTCTAAACAATAAATTT
QY	98 ATAGTGTTAATATTATCATAGGGTCATCAAAATGAAGCTTCTCCTTGGGCTGCATTGTA
DB	61 ATAGGTAAATATATCATAGGGTCATCAAAATGAAGCTTCTCCTTGGGCTGCATTGTA
QY	158 TGTGTTGCTTTTTCGAAGAGAGAGGTTCCCCCTCATTTGGAGAGATGACAAATGACAT
DB	121 TGTTGTGCTTTTTCGAAGAGAGAGGTTCCCCCTCATTTGGAGATGACAAATGACAT
QY	218 GGTCAACCACATTCATCTCTGTAATATTCCTTAGCATACGAAATTTACACCTCT
DB	181 GGTCACCACTTCATTCATCTCTGTAATATTCCTTAGCATACGAAATTTACACCTCT
QY	278 CTTTATTATCGGCCAGTGAAATACAGTCCCAGTTAACCTGGGAATATTACACTGACACA
DB	241 CTTTATTATCGGCCAGTGAAATACAGTCCCAGTTAACCTGGGAATATTACACTGACACA
QY	338 GGGTTACCTTGATACCCCTGATCTTTTAACTTCTCTGATATCCCTTATGTCTATGACATC
DB	301 GGGTTACCTTGATACCCCTGATCTTTTAACTTCTCTGATATCCCTTATGTCTATGACATC
QY	398 CGTGATTTTCCCTTAGTACTAGTATGTAATGTTCTCTCTCCCTCTAGAGGGATTCCCG
DB	361 CGTGATTTTCCCTTAGTACTAGTATGTAATGTTCTCTCTCCCTCTAGAGGGATTCCCG
QY	458 TTGTGCTCCTCTTCAAAGTTTTTTTTCAGACGCTGACAGACCCGCTGCCCACTTATGCA
DB	421 TTGTGCTCCTCTTCAAAGTTTTTTTTCAGACGCTGACAGACCCGCTGCCCACTTATGCA
QY	518 GCTAGACCTGCTGACGCTGACACCTTTTACAGCCACACCTGTATGACAGCTGACCTGCTGCA
DB	481 GCTAGACCTGCTGACGCTGACACCTTTTACAGCCACACCTGTATGACAGCTGACCTGCTGCA
QY	578 GGGGCCCCCTGTTGACGTGAGCCCTGCTGACAGAGGACCTGTTGAGAGCTGAGCCCTGCA
DB	541 GGGGCCCCCTGTTGACGTGAGCCCTGCTGACAGAGGACCTGTTGAGAGCTGAGCCCTGCA
QY	638 GAGGACACTGTTGACGTGAGCCCTGCTGACAGAGGACCTGTTGAGAGCTGAGCCACTGCA
DB	601 GAGGACACTGTTGACGTGAGCCCTGCTGACAGAGGACCTGTTGAGAGCTGAGCCACTGCA
QY	698 GAGGAACCTTACCAAGCTGAGCTGCTGACAGCCAAAGCCTGCTG 740

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Db      661 GAGGACCTTACCAGCTGAGCGCTGTACAGCCAGCCTGCTG 703
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ID HSM076010 standard; RNA; EST; 682 BP.
XX HSM076010 standard; RNA; EST; 682 BP.
XX BX485923;
XX BX485923.1
SV BX485923.1
DT 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
DB Homo sapiens mRNA; EST DKFP686L06248_r1 (from clone DKFP686L06248)
KW EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX
XX [1]
RN 1-682
RP Ottenmaier B., Obermaier B., Deutschenbauer S., Mewes H.W., Weil B.,
RA Amold C., Osanger A., Pobo G., Han W., Wiemann S.;
RL Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL MRS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
XX
XX This is the 5' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by Medigenomix (Martinried/Germany) within the CDNA
CC sequencing consortium of the German Genome Project.
CC No sl sequence available.
CC This clone (DKFP686L06248) is available at the RZPD in Berlin.
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH location/Qualifiers
FH
FH source
FT 1. 682
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFP686L06248"
FT /clone_1kb="686 (synonym: hlcc3). Vector psport1_sfi; host
FT DH10B; sites SfiIA + SfiIB"
FT /dev_stage="adult"
FT /tissue_type="CDNA-collection"
XX
SQ Sequence 682 BP; 141 A; 199 C; 150 G; 192 T; 0 other;
Query Match 67.5%; Score 680.4; DB 2; Length 682;
Best Local Similarity 99.9e+100; Pred. NO. 4.9e-100;
Matches 681; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 72 TGCGTATTTCTAAACAATTAATTATTTAGTGTTAATATTCATAGGGTCANTCAATAATGA 131
|||
DY 1 TGCCTATTTCTAAACAATTAATTATTTAGTGTTAATATTCATAGGGTCANTCAATAATGA 60
|||
DY 132 AGCTTCTCTTTGGGCGCTGATGTATGTGTGTTTGCAGAAGAGACGGTTCCCT 191
|||
DY Db 61 AGCTTCTCTTTGGGCGCTGATGTATGTGTGTTTGCAGAAGAGACGGTTCCCT 120
|||
DY 192 TCATTGTGAGATGACATGACGATGTCACCCACTTCATTCATCTCTGAATATTTCTT 251
|||
DY Db 121 TCATTGTGAGATGACATGACGATGTCACCCACTTCATTCATCTCTGAATATTTCTT 180
|||
DY 252 ATGCCATACGGAATTTCACACCTCTCTTTATATGSCCAAGTAATACGTCGCCAGTT 311
|||

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Db      181 ATGCATACGGAATTTACCACTCTCTTTATATGCCACGATGATACAGTCCCACTT 240
Qy      312 ACCCTGGAAATCTTACCTGACACAGGGTTACCTTGTATCCTTGATTTCTAATCTTC 371
Db      241 ACCCTGGAAATCTTACCTGACACAGGGTTACCTTGTATCCTTGATTTCTAATCTTC 300
Qy      372 CTGATTTCCCTATGTCATGACATCCGTTGTTTCCCTTAGCTACTAGTTGATGTTTC 431
Db      301 CTGATTTCCCTATGTCATGACATCCGTTGTTTCCCTTAGCTACTAGTTGATGTTTC 360
Qy      432 CTCCTCTCCCTCTTACGAGGGTTTCCGTTTGTCTCTCTTCAAGTTTCTTACAGAGCTG 491
Db      361 CTCCTCTCCCTCTTACGAGGGTTTCCGTTTGTCTCTCTTCAAGTTTCTTACAGAGCTG 420
Qy      492 CAGACCCGCTGCCCCACCTTATGTCAGTGTGAGCTGCTGACGCTGACCTTCTTACAGCA 551
Db      421 CAGACCCGCTGCCCCACCTTATGTCAGTGTGAGCTGCTGACGCTGACCTTCTTACAGCA 480
Qy      552 CACCTGTAGCAGCTGAGCTGCTGAGGGGCCCTGTTGACGCTGAGCTGAGCTGAGAGG 611
Db      481 CACCTGTAGCAGCTGAGCTGCTGAGGGGCCCTGTTGACGCTGAGCTGAGCTGAGAGG 540
Qy      612 CACCTGTAGCAGCTGAGCTGCTGAGGGGCCCTGTTGACGCTGAGCTGAGCTGAGAGG 671
Db      541 CACCTGTAGCAGCTGAGCTGCTGAGGGGCCCTGTTGACGCTGAGCTGAGCTGAGAGG 600
Qy      672 CACCTGTAGCAGCTGAGCTGCTGAGGGGCCCTGTTGACGCTGAGCTGAGCTGAGAGG 731
Db      601 CACCTGTAGCAGCTGAGCTGCTGAGGGGCCCTGTTGACGCTGAGCTGAGCTGAGAGG 660
Qy      732 AGCCGCTGCCCCGAACTCTCA 753
Db      661 AGCCGCTGCCCCGAACTCTCA 682

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RESULT 3
CB957562          742 bp  mRNA  linear  EST 29-APR-2003
LOCUS             CB957562
DEFINITION       CB957562.1 GI:30213679
ACCESSION        CB957562
VERSION          CB957562.1
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@dbp-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: NDCM151 row: j column: 01
High quality sequence stop: 551.
Location/Qualifiers
1. 742
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352440"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_184"
/notes="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccatcgcc); Site_2: SfiI (ggccgcccggcc);
Library is oligo-dT primed and directionally cloned. cDNA

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BASE COUNT 172 a 203 c 154 g 213 t

Query Match 67.2%; Score 677.4; DB 14; Length 742;  
Best Local Similarity 98.8%; Pred. No. 1.5e-99;  
Matches 714; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence: 5'-ATTCTAGAGCCCGAGGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

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Qy      1 AGACAGACTAAAAAGCAGTATTTCTTGTCTCTCTTAAAGAAAGAAATATATAT 60
Db      16 AGACAGACTAAAAAGCAGTATTTCTTGTCTCTCTTAAAGAAAGAAATATATAT 75
Qy      61 TAAAAATACATTTGGTATTTCTTAAACATTAATTAATAGTTAATATTCATAGGCTC 120
Db      76 TAAAAATACATTTGGTATTTCTTAAACATTAATTAATAGTTAATATTCATAGGCTC 135
Qy      121 AATCAAAATGAAGCTTCTCTTGGGCGCTGATTTATGTTATGTTGCTTTGCAAGAGAG 180
Db      136 AATCAAAATGAAGCTTCTCTTGGGCGCTGATTTATGTTATGTTGCTTTGCAAGAGAG 195
Qy      181 ACGGTTCCCTCTCATTTGATGAGATGACAAATGACATGATGTCACCACTTCATCCATCT 240
Db      196 ACGGTTCCCTCTCATTTGATGAGATGACAAATGACATGATGTCACCACTTCATCCATCT 255
Qy      241 GAATATTTCTTATGACATAGGAAATTTTACCACTCTCTTATATATGCCCCAGTAAATAC 300
Db      256 GAATATTTCTTATGACATAGGAAATTTTACCACTCTCTTATATATGCCCCAGTAAATAC 315
Qy      301 AGTCCCAAGTACCTGCGGAATCTTACCTGACACAGGGTTACTTCGTATCCCTGGAT 360
Db      316 AGTCCCAAGTACCTGCGGAATCTTACCTGACACAGGGTTACTTCGTATCCCTGGAT 375
Qy      361 TCTACTTCTCTGAGATTTCCCTATATGTCATACATCCGTTGTTTCCCTTAGCTACTCA 420
Db      376 TCTACTTCTCTGAGATTTCCCTATATGTCATACATCCGTTGTTTCCCTTAGCTACTCA 435
Qy      421 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db      436 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 495
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Db      496 TTACGACGCTGACAGACCCGCTGCCCCACCTATTTGACGCTGAGCTGCTGACGTCAGC 555
Qy      541 TCTTACAGCCACACTGTAGAGCTGAGCTGCTGACAGGGGCCCTGTGAGCTGAGGCC 600
Db      556 TCTTACAGCCACACTGTAGAGCTGAGCTGCTGACAGGGGCCCTGTGAGCTGAGGCC 615
Qy      601 TGCTGACAGGCACTGTTG3-AGCTGAGCTGCTGACAGGCACTGTTGACGCTAGC 659
Db      616 TGCTGACAGGCACTGTTG3AGCTGAGCTGAGCTGCTGACAGGCACTGTTGACGCTAGC 675
Qy      660 CTGCTGACAGGCACTGTTG-TTGAGTGTGAGGCACTGCTGACAGGAA-CTTTCACCACTGA 717
Db      676 CTGCTGACAGGCACTGTTGTGATGTGAACCCGCTGACAGAAACCTTTCACCACTGA 735
Qy      718 GCC 720
Db      736 GCC 738

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RESULT 4  
HSM075890  
ID HSM075890 standard; RNA; EST; 677 BP.

XX		BA485703;	
AC			
XX		BA485703.1	
SV			
XX		09-MAY-2003 (Rel. 75, Created)	
DT		09-MAY-2003 (Rel. 75, Last updated, Version 1)	
DE		Homo sapiens mRNA; EST DKFP66D09248_r1 (from clone DKFP66D09248)	
XX			
XX		EST; expressed sequence tag.	
KM			
XX		Homo sapiens (human)	
OS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia,	
OC		Eutheria; Primates; Catarrhini; Homnidae; Homo.	
CC			
XX		[1]	
RN		1-677	
RP		Ottewelselder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B.,	
RA		Amid C., Osanger A., Pobo G., Han W., Wiemann S.;	
RT		' Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases.	
RL		MRS, Ingelstaedter Landstr.1, D-85764 Neuberg, GERMANY	
XX		This is the 5' sequence of the clone insert	
CC		Clone from S. Wiemann, Molecular Genome Analysis, German Cancer	
CC		Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;	
CC		sequenced by Medigenomix (Martinried/Germany) within the CDNA	
CC		sequencing consortium of the German Genome Project.	
CC		No sl sequence available.	
CC		This clone (DKFP66D09248) is available at the RZPD in Berlin.	
CC		Please contact the RZPD: Ressourcencentrum, Heubnerweg 6,	
CC		14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de	
XX			
XX			
FH	Key	Location/Qualifiers	
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	Query Match	66.2%; Score 667; DB 2; Length 677;	
	Best Local Similarity	100.0%; Pred. NO. 7e-98;	
	Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY		3 ACAGACTAAAAAACCAGATGATTCTTCGTCTCTCTTAAGAAGAAATAATTA 62	
Db		11 ACAAGCTAAAACCAAGTATTTCTTCGTCTCTCTTAAGAAGAAATAATTA 70	
QY		63 AAAATACATTCGGTATTTCTTAAACAATAATTATAGTGAATTCATAGGCTCA 122	
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QY		123 TCAGAAATGAAGCTCTCCTTTGGGCCCTGCATGTATGTGTTGCTTTGCAAGAGAGAC 182	
Db		131 TCAAAATGAAGCTCTCCTTTGGGCCCTGCATGTATGTGTTGCTTTGCAAGAGAGAC 190	
QY		183 GGTTCCCCCTCATTTGGTAGGATGACATGACATGGTCAACCCACTCATTCATCTCGA 242	
Db		191 GGTTCCCCCTCATTTGGTAGGATGACATGACATGGTCAACCCACTCATTCATCTCGA 250	
QY		243 ATATTCTTATGCAATGCAATTTACCACTCTCTTATATATGCCCAGTGAAATCAG 302	
Db		251 ATATTCTTATGCAATGCAATTTACCACTCTCTTATATATGCCCAGTGAAATCAG 310	
QY		303 TCCCCAGTTACCTGGGAATCTTACACTGACACAGGGTTACCTTGATTCCTGATTC 362	

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Db      311  TCCCACTTACCTGGGAATACCTTACAGACAGAGGTTACCTTGATCCCTGGATTC 370
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Oy      423  TGAATGTTCCCTCCCTCCCTCCAGAGGGTTTCCCGTTTGCCCTCTTCAAGGTTTTTT 482
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Oy      483  CAGCAGCTGAGAGCACCCTGCTGCCCACTATTGACACTGAGCTGACGTGACCTC 542
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Db      551  TTACAGCCCAACCTGTATGACAGCTGAGCTGCTGACAGGGGCCCTGTTGACAGTGA 610
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Db      611  CTGACAGAGGACCTGTTTGAGCTGAGCCTGCTGACAGAGGACCTGTTGAGCTGAG 670
Oy      663  CTGACAGA 669
Db      671  CTGACAGA 677

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ID      HSM075629 strand, RNA; EST; 669 BP.
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XX      SV      BX485442.1
DT      09-MAY-2003 (Rel. 75, Created)
DT      09-MAY-2003 (Rel. 75, Last updated, Version 1)
DE      Homo sapiens mRNA; EST DKFZp686D11247_r1 (from clone DKFZp686D11247)
XX      EST, expressed sequence tag.
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia
OC      Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN      [1]
RP      1-669
RA      Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA      Han W., Wiemann S.;
RT      Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Ingolstraedter Landstr.1, D-85764 Neuherberg, GERMANY
CC      This is the 5' sequence of the clone insert
CC      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC      Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC      sequenced by QIAGEN (Hilden/Germany) within the CDNA sequencing
CC      consortium of the German Genome Project.
CC      No sl sequence available.
CC      This clone (DKFZp686D11247) is available at the RZPD in Berlin.
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC      14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
FH      Key      Location/Qualifiers
FT      source      1..669
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OY		610	GGCACCTGTTGAGAGCTGAGCCTGCTGCAGAGGCAACCTGTTTGACAGTGAAGCTTCT	664
Db		623	GGCACCTGTTGAGAGCTGAGCCTGCTGCAGAGGCAACCTGTTTGACAGTGAAGCTTCT	677
 RESULT 7 HSM076755 standard; RNA; EST; 675 BP.				
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AC		BX486568;		
SV		BX486568.1		
XX		09-MAY-2003 (Rel. 75, Created)		
DT		09-MAY-2003 (Rel. 75, Last updated, Version 1)		
DE		Homo sapiens mRNA; EST DKFP686H08252_r1 (from clone DKFP686H08252)		
XX		EST; expressed sequence tag.		
KW		Homo sapiens (human)		
OC		Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia		
OC		Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
XX		[1]		
RP		1-675		
BA		Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Podo G.,		
RA		Han W., Wiemann S.;		
RT		; Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases.		
RL		MRS., Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY		
XX		This is the 5' sequence of the clone insert		
CC		Clone from S. Wiemann, Molecular Genome Analysis, German Cancer		
CC		Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;		
CC		sequenced by Qigen (Hilden/Germany) within the cDNA sequencing		
CC		consortium of the German Genome Project.		
CC		No al sequence available.		
CC		This clone (DKFP686H08252) is available at the RZPD in Berlin.		
CC		Please contact the RZPD: Ressourcententrum, Heubnerweg 6,		
CC		14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de		
Key		Location/Qualifiers		
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Query Match		64.9%; Score 654.6; DB 2; Length 675;		
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Matches		668; Conservative 0; Mismatches 4; Indels 1; Gaps 1;		
OY		68 ACATTGGCATATTTCTAAACAATPAATAATTAAGTAGTAAATATCAT-AGGGTCATCA	126	
Db		3 ACATTGGCATATTTCTAAACAATPAATAATTAAGTAGTAAATATCATAGGTCATCA	62	
OY		127 AATGAAGCTTCTCCCTTTGGGCGCTGCATGTATGTGTGCTTTTCCAAGAAGACCGTT	186	
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OY		187 CCCCTTCAATGGTAGATGACATGACGATGTCACCCACTTCAATCATCTCTGAATAT	246	

Df		123	Ccccttcatttgatgagatgacgaatagcgatggtaaccacttcatcctctaataat	182		
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Dd		183	TcctttatggcatnrcgaaATTYACCACTTCCTCTTYATA TGTGCCCCAGTAACAGTCCC	242		
Oy		307	cagttAACCCGGGAATAACTTACACTGACA GAGGGTTA CTTTGTAATCCCTGAA TTC TAAC	366		
Dd		243	CAGTTAACCCGGGAATAACTTACACTGACA GAGGGTTA CTTTGTAATCCCTGAA TTC TAAC	302		
Oy		367	tTCTCTGTGATTC CCCTATGTCTATCACATCCG GTGTTTTGCC TTAGTACTAGTTGAA	426		
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Dd		483	AGCCACACCTGTATG ACGCTGAGCCTCTG ACAGGGGCC CCTGTGTG CAGCTAGCCTGTGC	542		
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Dd		543	AGAAGCACCTGTGTG AGACTGAGCCTGTG CA GAAGGCA CTTGTGTG CAGCTGAGCCTGTGC	602		
Oy		667	AGAAGCACCTGTGTG AGACTGAGCCTGTG CA GAAGGCA CTTGAC CAGCTGAGCCTGTGC	726		
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Dd		663	AGCCAGCCTGTCT 675 			
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ID	HSM076748	standard; RNA; EST; 675 BP.				
AC	BX486561;					
XX	XX					
SV	BX486561.1					
DT	09-MAY-2003 (Rel. 75, Created)					
XT	09-MAY-2003 (Rel. 75, Last updated, Version 1)					
DE	Homo sapiens mRNA; EST DKFPZP686H20252_r1 (from clone DKFPZP686H20252)					
XX	EST, expressed sequence tag.					
OS	Homo sapiens (human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia					
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.					
XX	[1]					
Rf	1-675					
RA	Bahr A., Lauber J., Mewes H.W., Well B., Amid C., Oeanger A., Fobo G.,					
RT	Han W., Wiemann S.;					
RL	Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases. MIRS, Ingelstaedter Landstr.1, D-85764 Neuherberg, GERMANY					
CC	This is the 5' sequence of the clone insert					
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer					
CC	Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;					
CC	sequenced by QIAGEN (Hilden/Germany) within the cDNA sequencing					
CC	consortium of the German Genome Project.					
CC	No fl sequence available.					



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QY 301 AGTCCCGATTACCTGGGAATATTACAGTACAGAGGTTACCTGATCCCTGAT 360
DB 312 AGTCCCGATTACCTGGGAATATTACAGTACAGAGGTTACCTGATCCCTGAT 371
QY 361 TCTAATCTCTCTGATTTCCCTATGCTATACATCCGTTGTTTCCCTTAGTACTCA 420
DB 372 TCTAATCTCTCTGATTTCCCTATGCTATACATCCGTTGTTTCCCTTAGTACTCA 431
QY 421 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
DB 432 GTTGAATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491
QY 481 TTCACAGCTGACAGCCGCTGACCCCACTATGACGTGACCTGACGTGACCC 540
DB 492 TTCACAGCTGACAGCCGCTGACCCCACTATGACGTGACCTGACGTGACCC 551
QY 541 TCTTACAGCCACCTGTTAGCAGCTGAGCTGCTGCAAGAGGACCTGTTGACGCT 600
DB 552 TCTTACAGCCACCTGTTAGCAGCTGAGCTGCTGCAAGAGGACCTGTTGACGCT 611
QY 601 TGCTGCAAGGACCTGTTGAGCTGAGCTGCTGCTGCAAGAGGACCTGTTGACGCT 655
DB 612 TGCTGCAAGGACCTGTTGAGCTGAGCTGCTGCTGCAAGAGGACCTGTTGACGCT 665

RESULT 10
HSM077932 standard; RNA; EST; 678 BP.
AC BX487745;
XX BX487745.1
XX 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp686N16258_r1 (from clone DKFZp686N16258)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
RN 1-678
RA Bahr J., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL M18, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX This is the 5' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
CC consortium of the German Genome Project.
CC No. 61 sequence available.
CC This clone (DKFZp686N16258) is available at the RZPD in Berlin.
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
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FT /mol_type="mRNA"
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Query Match 63.5%; Score 640.4; DB 2; Length 678;
Best Local Similarity 99.5%; Pred. No. 1.4e-93;
Matches 652; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 85 TAAATATCATTTGCTATTTCTAAACATATTAATAGTTATATTCATAGGCTC 144
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DB 145 AATCAAAATGAAGCTTCTCTTTGGGCTGATATGATGTTGTTTGCAGGAAG 204
QY 181 AAGGTTCCCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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QY 601 TGCTGCAAGGACCTGTTGAGCTGAGCTGCTGCTGCAAGAGGACCTGTTGACGCT 655
DB 624 TGCTGCAAGGACCTGTTGAGCTGAGCTGCTGCTGCAAGAGGACCTGTTGACGCT 678

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AC BX487670;
XX BX487670.1
XX 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp686G13258_r1 (from clone DKFZp686G13258)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
RN 1-647

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QY 181 ACGTTTCCCTTCATTTGGTGGAGATGACAGATGTCACCGACTTCATCCATCTCT 240
Db 193 ACGTTTCCCTTCATTTGGTGGAGATGACAGATGTCACCGACTTCATCCATCTCT 252
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Db 253 GAATATTCCTTATGAGCATACGGAATTTTACACCTCTCTTATATTCGCCAGTAATAC 312
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Db 313 AGTCCCAAGTAACTCGGAAATATTAACAAGTGAACAGAGTTTACCTTGGATCCCTGAT 372
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RESULT 13  
HSM075827 standard; RNA; EST; 658 BP.

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SV BX485640.1
XX 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp686p12247_r1 (from clone DKFZp686p12247)
DE EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN Bahr A., Lauber J., Mewes H.W., Weill B., Amid C., Osanger A., Podo G.,
RP Han W., Wiemann S.;
RA Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RT MIPB, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
RL MIPB, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX This is the 5' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
CC consortium of the German Genome Project.
CC No 5' sequence available.
CC This clone (DKFZp686p12247) is available at the RZPD in Berlin.
CC Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
XX Key Location/Qualifiers
FH source 1. 658
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SQ Sequence 658 BP; 159 A; 173 C; 124 G; 202 T; 0 other;
Query Match 60.0%; Score 605; DB 2; Length 658;
Best Local Similarity 100.0%; Pred. No. 7e-88;
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TAAAAATCATTTGGTATTTCTTAAACATTAATTAATTAATTAATTAATTAATTAATTA 120
Db 114 TAAAAATCATTTGGTATTTCTTAAACATTAATTAATTAATTAATTAATTAATTAATTA 173
QY 121 AATCAAAATGAAGCTTCTCTTGGGCTGATGATGATGATGATGATGATGATGATGATG 180
Db 174 AATCAAAATGAAGCTTCTCTTGGGCTGATGATGATGATGATGATGATGATGATGATG 233
QY 181 ACGTTTCCCTTCATTTGGTGAATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 224 ACGTTTCCCTTCATTTGGTGAATGATGATGATGATGATGATGATGATGATGATGAT 293
QY 241 GAATATTCCTTATGAGCATACGGAATTTTACACCTCTCTTATTAATGAGCCAGTAATAC 300
Db 294 GAATATTCCTTATGAGCATACGGAATTTTACACCTCTCTTATTAATGAGCCAGTAATAC 353
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Db 354 AGTCCCAAGTAACTCGGAAATATTAACAAGTGAACAGAGTTTACCTTGGATCCCTGAT 413
QY 361 TCTAATCTCTCTGATATTCCTTATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 414 TCTAATCTCTCTGATATTCCTTATGATGATGATGATGATGATGATGATGATGATGAT 473
QY 421 GTTGAATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 474 GTTGAATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 533
QY 481 TTACAGCAGCTGAGACACCGCTGCTCCCACTATGTCAGCTGAGCTGCTGAGCTGAC 540
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QY 541 TCTTACAGCAGCAGCTGAGCAGCTGAGCAGCTGAGCAGCAGCAGCAGCAGCAGCAG 600
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Db 654 TGTCTG 658

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RESULT 14  
HSM074630 standard; RNA; EST; 618 BP.

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XX HSM074630 standard; RNA; EST; 618 BP.
AC BX484444.1
SV BX484444.1
XX 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp686A01243_r1 (from clone DKFZp686A01243)
DE
XX

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QY 71 TTGGTATTTCATAAACATTAATTATAGCTTAATATTCATAGGCTCATCAAAATG 130  
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Db 84 TTGGTATTTCATAAACATTAATTATAGCTTAATATTCATAGGCTCATCAAAATG 143  
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QY 131 AAGCTTCCTTTGGGGCTGATGTATGTGTGCTTTGCAAGGAAGAGAGGTTCCCG 190  
|||  
Db 144 AAGCTTCCTTTGGGGCTGATGTATGTGTGCTTTGCAAGGAAGAGAGGTTCCCG 203  
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QY 191 TTCATTGGTGAAGATGACATGACGATGTACACCCACTTCATCCATCTGTGAATATTCCT 250  
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Db 204 TTCATTGGTGAAGATGACATGACGATGTACACCCACTTCATCCATCTGTGAATATTCCT 263  
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QY 251 TATGGCATACGGAATTTACCACTCTCTTTATATGCGCCAGTGAATACAGTCCCGAGT 310  
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Db 264 TATGGCATACGGAATTTACCACTCTCTTTATATGCGCCAGTGAATACAGTCCCGAGT 323  
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QY 311 TACCCTGGGAATPACTTACACTGACACAGGGTTACCTGTATCCCTGATTCCTTAATTCT 370  
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Db 324 TACCCTGGGAATPACTTACACTGACACAGGGTTACCTGTATCCCTGATTCCTTAATTCT 383  
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QY 371 CCTGGATTCCCTATGTCTATCAATCCGTGGTTTCCTTAGCTACTCAGTTGAATGTT 430  
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Db 384 CCTGGATTCCCTATGTCTATCAATCCGTGGTTTCCTTAGCTACTCAGTTGAATGTT 443  
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QY 431 CCTCTCTCCCTCTAGGGGTTTCCCGTTTGTCCCTCTCAAGGTTTTTTTCAAGAGCT 490  
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Db 444 CCTCTCTCCCTCTAGGGGTTTCCCGTTTGTCCCTCTCAAGGTTTTTTTCAAGAGCT 503  
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QY 491 GCAGACCCCGCTGCCCACTTATGACGTGAGCTGCGAGCTGCACTTACAGCC 550  
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Db 504 GCAGACCCCGCTGCCCACTTATGACGTGAGCTGCGAGCTGCACTTACAGCC 563  
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QY 551 ACACCTGTAGCACTGAGCTGCTGCAAGGGGCCCTGTGCACTGA 597  
|||  
Db 564 ACACCTGTAGCACTGAGCTGCTGCAAGGGGCCCTGTGCACTGA 610  
|||

Search completed: January 16, 2004, 09:22:47  
Job time : 2135 secs